

```

<110> Genentech, Inc.
      Ashkenazi, Avi
      Botstein, David
      Desnoyers, Luc
      Eaton, Dan L.
      Ferrara, Napoleone
      Filvaroff, Ellen
      Fong, Sherman
      Gao, Wei-Qiang
      Gerber, Hanspeter
      Gerritsen, Mary E.
      Goddard, A.
      Godowski, Paul J.
      Grimaldi, Christopher J.
      Gurney, Austin L.
      Hillan, Kenneth, J.
      Kljavin, Ivar J.
      Mather, Jennie P.
      Pan, James
      Paoni, Nicholas F.
      Roy, Margaret Ann
      Stewart, Timothy A.
      Tumas, Daniel
      Williams, P. Mickey
      Wood, William, I.

<120> Secreted and Transmembrane Polypeptides and Nucleic
      Acids Encoding the Same

<130> 10466-14

<140> 09/665,350
<141> 2000-09-18

<150> PCT/US00/04414
<151> 2000-02-22

<150> US 60/143,048
<151> 1999-07-07

<150> US 60/145,698
<151> 1999-07-26

<150> US 60/146,222
<151> 1999-07-28

<150> PCT/US99/20594
<151> 1999-09-08

<150> PCT/US99/20944
<151> 1999-09-13

```

<150> PCT/US99/21090  
<151> 1999-09-15

<150> PCT/US99/21547  
<151> 1999-09-15

<150> PCT/US99/23089  
<151> 1999-10-05

<150> PCT/US99/28214  
<151> 1999-11-29

<150> PCT/US99/28313  
<151> 1999-11-30

<150> PCT/US99/28564  
<151> 1999-12-02

<150> PCT/US99/28565  
<151> 1999-12-02

<150> PCT/US99/30095  
<151> 1999-12-16

<150> PCT/US99/30911  
<151> 1999-12-20

<150> PCT/US99/30999  
<151> 1999-12-20

<150> PCT/US00/00219  
<151> 2000-01-05

<160> 423

<210> 1

<211> 1825

<212> DNA

<213> Homo sapiens

<400> 1

```
actgcacctc ggttctatcg attgaattcc ccgggggatcc tctagagatc cctcgacctc 60
gacccacgcg tccggggccgg agcagcacgg ccgcaggacc tggagctccg gctgcgcttt 120
cccgagcgcg taccgcgcat gcgcctgccg cgccggggccg cgctggggct cctgccgctt 180
ctgctgctgc tgccgcccgc gccggaggcc gccaaagaagc cgacgcccctg ccaccgggtgc 240
cggggggctgg tggacaagtt taaccagggg atggtggaca ccgcaaagaa gaactttggc 300
ggcggaaca cggtttggga ggaaaagacg ctgtccaagt acgagtccag cgagattcgc 360
ctgctggaga tcctggaggg gctgtgagag agcagcgact tcgaatgcaa tcagatgcta 420
gaggcgcagg aggagcacct ggaggcctgg tggctgcagc tgaagagcga atatcctgac 480
ttattcgagt ggttttgtgt gaagacactg aaagtgtgct gctctccagg aacctacggt 540
cccgaactgtc tcgcatgccg gggcggatcc cagaggccct gcagcgggaa tggccactgc 600
agcggagatg ggagcagaca gggcgacggg tcctgcccgt gccacatggg gtaccagggc 660
```

```
<210> 2
<211> 353
<212> PRT
<213> Homo sapiens
```

<400>	2															
Met	Arg	Leu	Pro	Arg	Arg	Ala	Ala	Leu	Gly	Leu	Leu	Pro	Leu	Leu	Leu	
1				5					10						15	
Leu	Leu	Pro	Pro	Ala	Pro	Glu	Ala	Ala	Lys	Lys	Pro	Thr	Pro	Cys	His	
			20					25					30			
Arg	Cys	Arg	Gly	Leu	Val	Asp	Lys	Phe	Asn	Gln	Gly	Met	Val	Asp	Thr	
		35					40					45				
Ala	Lys	Lys	Asn	Phe	Gly	Gly	Gly	Asn	Thr	Ala	Trp	Glu	Glu	Lys	Thr	
	50					55					60					
Leu	Ser	Lys	Tyr	Glu	Ser	Ser	Glu	Ile	Arg	Leu	Leu	Glu	Ile	Leu	Glu	
65					70					75					80	
Gly	Leu	Cys	Glu	Ser	Ser	Asp	Phe	Glu	Cys	Asn	Gln	Met	Leu	Glu	Ala	
				85					90						95	
Gln	Glu	Glu	His	Leu	Glu	Ala	Trp	Trp	Leu	Gln	Leu	Lys	Ser	Glu	Tyr	
			100					105					110			
Pro	Asp	Leu	Phe	Glu	Trp	Phe	Cys	Val	Lys	Thr	Leu	Lys	Val	Cys	Cys	
		115					120					125				
Ser	Pro	Gly	Thr	Tyr	Gly	Pro	Asp	Cys	Leu	Ala	Cys	Gln	Gly	Gly	Ser	
	130					135					140					

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
 145 150 155 160  
 Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
 165 170 175  
 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
 180 185 190  
 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
 195 200 205  
 Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
 210 215 220  
 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
 225 230 235 240  
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
 245 250 255  
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
 260 265 270  
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
 275 280 285  
 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
 290 295 300  
 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
 305 310 315 320  
 Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala  
 325 330 335  
 Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp  
 340 345 350

Leu

<210> 3

<211> 2206

<212> DNA

<213> Homo sapiens

<400> 3

cagggtccaac tgcacctcgg ttctatcgat tgaattcccc ggggatcctc tagagatccc 60  
 tcgacctoga cccacgcgtc cgccaggccg ggaggcgacg cgcccagccg tctaaacggg 120  
 aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180  
 ggtgcggcac gaggagtttt cccggcagcg aggaggtcct gagcagcatg gcccggagga 240



ggcgccttccc tgccgcgcgcg ctctggctct ggagcatcct cctgtgcctg ctggcaactgc 300  
 gggcggaggc cgggcccgcg caggaggaga gcctgtacct atggatcgat gctcaccagg 360  
 caagagtact cataggattt gaagaagata tcctgattgt ttcagagggg aaaatggcac 420  
 cttttacaca tgatttcaga aaagcgcaac agagaatgcc agctattcct gtcaatatcc 480  
 attccatgaa ttttacctgg caagctgcag ggcaggcaga atacttctat gaattcctgt 540  
 ccttgcgctc cctggataaa ggcatcatgg cagatccaac cgtcaatgtc cctctgctgg 600  
 gaacagtgcc tcacaaggca tcagttgttc aagtgtgttt cccatgtctt ggaaaacagg 660  
 atgggggtggc agcatttgaa gtggatgtga ttgttatgaa ttctgaaggc aacaccattc 720  
 tccaaacacc tcaaaatgct atcttcttta aaacatgtca acaagctgag tgcccaggcg 780  
 ggtgccgaaa tggaggcttt tgtaatgaaa gacgcactcg cgagtgtcct gatgggttcc 840  
 acggacctca ctgtgagaaa gccctttgta cccacgatg tatgaatggg ggactttgtg 900  
 tgactcctgg tttctgcac tgcccacctg gattctatgg agtgaactgt gacaaagcaa 960  
 actgctcaac cacctgcttt aatggaggga cctgtttcta cctggaaaa tgtatttgcc 1020  
 ctccaggact agagggagag cagtgtgaaa tcagcaaatg cccacaacc tgctgaaatg 1080  
 gaggtaaatg catttggtaaa agcaaatgta agtgttccaa aggttaccag ggagacctct 1140  
 gttcaaagcc tgtctgcgag cctggctgtg gtgcacatgg aacctgccat gaacccaaca 1200  
 aatgccaatg tcaagaaggt tggcatggaa gacactgcaa taaaaggtag gaagccagcc 1260  
 tcatacatgc cctgaggcca gcaggcgccc agctcaggca gcacacgcct tcaacttaaaa 1320  
 agggcgagga gcggcgggat ccacctgaat ccaattacat ctggtgaact ccgacatctg 1380  
 aaacgtttta agttacacca agttcatagc ctttggttaac ctttcatgtg ttgaatgttc 1440  
 aaataatggt cattacactt aagaatactg gcctgaattt tattagcttc attataaatc 1500  
 actgagctga tatttactct tccttttaag ttttctaagt acgtctgtag catgatggta 1560  
 tagattttct tgtttcagtg ctttgggaca gattttatat tatgtcaatt gatcagggtta 1620  
 aaattttcag tgtgtagtgt gcagatatct tcaaaaattac aatgcattta tgggtgtctgg 1680  
 gggcagggga acatcagaaa ggtaaatttg ggcaaaaatg cgtaagtcac aagaatttgg 1740  
 atggtgcagt taatgttgaa gttacagcat ttcagatttt attgtcagat atttagatgt 1800  
 ttgttacatt tttaaaaatt gctcttaatt tttaaactct caatacaata tattttgacc 1860  
 ttaccattat tccagagatt cagtattaaa aaaaaaaaaa ttacactgtg gtagtggcat 1920  
 ttaaacaata taatatattc taaacacaat gaaataggga atataatgta tgaacttttt 1980  
 gcattggctt gaagcaatat aatatattgt aaacaaaaca cagctcttac ctaataaaca 2040  
 ttttatactg tttgtatgta taaaataaag gtgctgcttt agtttttttg aaaaaaaaaa 2100  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcggccgc gactctagag tcgacctgca 2160  
 gaagcttggc cgccatggcc caacttgttt attgcagctt ataatg 2206

<210> 4

<211> 379

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser  
 1 5 10 15

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln  
 20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

65					70					75				80
Pro	Val	Asn	Ile	His	Ser	Met	Asn	Phe	Thr	Trp	Gln	Ala	Ala	Gly Gln
				85					90					95
Ala	Glu	Tyr	Phe	Tyr	Glu	Phe	Leu	Ser	Leu	Arg	Ser	Leu	Asp	Lys Gly
			100					105					110	
Ile	Met	Ala	Asp	Pro	Thr	Val	Asn	Val	Pro	Leu	Leu	Gly	Thr	Val Pro
		115					120					125		
His	Lys	Ala	Ser	Val	Val	Gln	Val	Gly	Phe	Pro	Cys	Leu	Gly	Lys Gln
	130					135					140			
Asp	Gly	Val	Ala	Ala	Phe	Glu	Val	Asp	Val	Ile	Val	Met	Asn	Ser Glu
145					150					155				160
Gly	Asn	Thr	Ile	Leu	Gln	Thr	Pro	Gln	Asn	Ala	Ile	Phe	Phe	Lys Thr
			165						170					175
Cys	Gln	Gln	Ala	Glu	Cys	Pro	Gly	Gly	Cys	Arg	Asn	Gly	Gly	Phe Cys
			180					185					190	
Asn	Glu	Arg	Arg	Ile	Cys	Glu	Cys	Pro	Asp	Gly	Phe	His	Gly	Pro His
		195					200					205		
Cys	Glu	Lys	Ala	Leu	Cys	Thr	Pro	Arg	Cys	Met	Asn	Gly	Gly	Leu Cys
	210					215					220			
Val	Thr	Pro	Gly	Phe	Cys	Ile	Cys	Pro	Pro	Gly	Phe	Tyr	Gly	Val Asn
225					230					235				240
Cys	Asp	Lys	Ala	Asn	Cys	Ser	Thr	Thr	Cys	Phe	Asn	Gly	Gly	Thr Cys
				245					250					255
Phe	Tyr	Pro	Gly	Lys	Cys	Ile	Cys	Pro	Pro	Gly	Leu	Glu	Gly	Glu Gln
			260					265					270	
Cys	Glu	Ile	Ser	Lys	Cys	Pro	Gln	Pro	Cys	Arg	Asn	Gly	Gly	Lys Cys
	275						280					285		
Ile	Gly	Lys	Ser	Lys	Cys	Lys	Cys	Ser	Lys	Gly	Tyr	Gln	Gly	Asp Leu
	290					295					300			
Cys	Ser	Lys	Pro	Val	Cys	Glu	Pro	Gly	Cys	Gly	Ala	His	Gly	Thr Cys
305					310					315				320
His	Glu	Pro	Asn	Lys	Cys	Gln	Cys	Gln	Glu	Gly	Trp	His	Gly	Arg His
				325					330					335
Cys	Asn	Lys	Arg	Tyr	Glu	Ala	Ser	Leu	Ile	His	Ala	Leu	Arg	Pro Ala
			340					345					350	

T00740"57920660

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu  
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp  
 370 375

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 5

agggagcacg gacagtgtgc agatgtggac gagtgtcac tagca

45

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 6

agagtgtatc tctggctacg c

21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 7

taagtccggc acattacagg tc

22

<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 8

cccacgatgt atgaatggtg gactttgtgt gactcctggt ttctgcatc

49

"090614 0400"  
 090614 0400

```

<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 9
aaagacgcat ctgcgagtgt cc                                     22

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 10
tgctgatttc aactgctct ccc                                     23

<210> 11
<211> 2197
<212> DNA
<213> Homo sapiens

<400> 11
cggacgcgtg ggcgtccggc ggtcgcagag ccaggaggcg gaggcgcgcg ggccagcctg 60
ggccccagcc cacaccttca ccaggggcca ggagccacca tgtggcgatg tccactgggg 120
ctactgctgt tgctgccgct ggctggccac ttgggtctgg gtgccagca gggtcgtggg 180
cgccgggagc tagcaccggg tctgcacctg cggggcatcc gggacgcggg aggccggtac 240
tgccaggagc aggacctgtg ctgcgcgggc cgtgccagcg actgtgccct gccctacctg 300
ggcgccatct gttactgtga cctcttctgc aaccgcacgg tctccgactg ctgccctgac 360
ttctgggact tctgcctcgg cgtgccaccc ccttttcccc cgatccaagg atgtatgcat 420
ggaggtcgtg tctatccagt cttgggaacg tactgggaca actgtaaccg ttgcacctgc 480
caggagaaca ggcagtggca tgggtggatc agacatgatc aaagccatca accagggcaa 540
ctatggctgg caggctggga accacagcgc cttctggggc atgacctgg atgagggcat 600
tcgctaccgc ctgggcacca tccgcccata ttctcgggtc atgaacatgc atgaaattta 660
tacagtgtct aacccagggg aggtgcttcc cacagccttc gaggcctctg agaagtggcc 720
caacctgatt catgagcctc ttgaccaagg caactgtgca ggctcctggg ccttctccac 780
agcagctgtg gcatccgata gtgtctcaat ccattctctg ggacacatga cgcctgtcct 840
gtcgcgccag aacctgctgt cttgtgacac ccaccagcag cagggtgcc gccgtggggc 900
tctcgatggt gcctggtggt tcctgcgtcg ccgaggggtg gtgtctgacc actgctaccc 960
cttctcgggc cgtgaacgag acgaggtctg ccctgcgccc ccctgtatga tgcacagccg 1020
agccatgggt cggggcaagc gccaggccac tgcccactgc cccaacagct atgttaataa 1080
caatgacatc taccaggtca ctctctgtcta ccgcctcggc tccaacgaca aggagatcat 1140
gaaggagctg atggagaatg gccctgtcca agccctcatg gaggtgcatg aggacttctt 1200
cctatacaag ggaggcatct acagccacac gccagtgagc cttgggaggc cagagagata 1260
ccqccqccat qggacccact caqtcaagat cacaggatgg ggagaggaga cgctgccaga 1320

```

```
<210> 12
<211> 164
<212> PRT
<213> Homo sapiens
```

Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Leu Pro Leu Ala Gly  
1 5 10 15

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys  
35 40 45

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
65 70 75 80

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr  
100 105 110

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln  
130 135 140

His Asp Pro Gly

<210> 13  
 <211> 533  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (33)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (80)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (94)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (144)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (188)  
 <223> a, t, c or g

<400> 13  
 aggctccttg gccctttttc cacagcaagc ttntgcnatc ccgattcggt gtctcaaatac 60  
 caattctctt gggacacatn acgcctgtcc tttingcccca gaacctgctg tcttgtacac 120  
 ccaccagcag cagggctgcc gcgntgggcg tctcgatggt gcctggtggt tcctgcgtcg 180  
 ccgagggntg gtgtctgacc actgctaccc cttctcgggc cgtgaacgag acgagggctgg 240  
 ccctgcgccc ccctgtatga tgcacagccg agccatgggt cggggcaagc gccaggccac 300  
 tgcccactgc cccaacagct atgttaataa caatgacatc taccagggtca ctctgtcta 360  
 ccgcctcggc tccaacgaca aggagatcat gaaggagctg atggagaatg gccctgtcca 420  
 agccctcatg gaggtgcatg aggacttctt cctatacaag ggaggcatct acagccacac 480  
 gccagtgagc cttgggaggc cagagagata ccgcggcat gggacccact cag 533

<210> 14  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 14

ttcgaggcct ctgagaagtg gccc

24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 15

ggcgggtatct ctctggcctc cc

22

<210> 16

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 16

ttctccacag cagctgtggc atccgatcgt gtctcaatcc attctctggg

50

<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

gctgcttgcc ctgttgatgg caggcttggc cctgcagcca ggcactgccc tgctgtgcta 60  
ctcctgcaaa gccaggtga gcaacgagga ctgcctgcag gtggagaact gcacccagct 120  
gggggagcag tgctggaccg cgcgcacccg cgcagttggc ctctgaccg tcatcagcaa 180  
aggctgcagc ttgaactgcg tggatgactc acaggactac tacgtgggca agaagaacat 240  
cacgtgctgt gacaccgact tgtgcaacgc cagcggggcc catgcctgc agccggctgc 300  
cgccatcctt gcgctgctcc ctgcaactcg cctgctgctc tggggacccg gccagctata 360  
ggctctgggg ggccccgctg cagccacac tgggtgtggt gccccaggcc tctgtgccac 420  
tcctcacaga cctggcccag tgggagcctg tcttggttcc tgaggcacat cctaacgcaa 480  
gtctgaccat gtatgtctgc acccctgtcc cccaccctga ccttcccatg gccctctcca 540  
ggactccac ccggcagatc agctctagtg acacagatcc gcctgcagat ggccccctcca 600  
accctctctg ctgctgtttc catggcccag cattctccac ccttaaccct gtgctcaggc 660  
acctcttccc ccaggaagcc ttccctgccc accccatcta tgacttgagc caggctctgg 720  
ccgtgggtgc ccccgacccc agcaggggac aggcactcag gaggggccag taaaggctga 780  
gatgaagtgg actgagtaga actggaggac aagagtcgac gtgagttcct gggagtctcc 840  
agagatgggg cctggaggcc tggaggaagg ggccaggcct cacattcgtg gggctccctg 900  
aatggcagcc tgagcacagc gtaggccctt aataaacacc tggttgataa gccaaaaaaa 960

<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

&lt;400&gt; 18

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val  
 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu  
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
 180 185

&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctcctgcaaa gccc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA





&lt;400&gt; 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

28

&lt;210&gt; 25

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
 gcggatctgc cgctgctca nctggtcggt catggcgccc t 41

<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 acttgccatc acctgttgcc agtgtggaaa aattctccct gttgaatddd ttgcacatgg 60  
 aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120  
 ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180  
 tccagtcatt ttgattttgc tgtttatddd ttttttcttt ttctttttcc caccacattg 240  
 tattttatddd ccgtacttca gaaatgggccc tacagaccac aaagtggccc agccatgggg 300  
 ctttttttcc gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360  
 tcctggcctg ccctagtgtg tgccgctgcg acaggaaactt tgtctactgt aatgagcgaa 420  
 gcttgacctc agtgccctctt gggatcccg agggcgtaac cgtactctac ctccacaaca 480  
 accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtcg gtgcacacgg 540  
 tctacctgta tggcaaccaa ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600  
 ttctccattt gcaggaaaac aatattcaga ccatttcacg ggctgctctt gccagctct 660  
 tgaagcttga agagctgcac ctggatgaca actccatata cacagtgggg gtggaagacg 720  
 gggccttccg ggaggctatt agcctcaaat tgtgttttt gtctaagaat cacctgagca 780  
 gtgtgcctgt tgggcttccct gtggacttgc aagagctgag agtggatgaa aatcgaattg 840  
 ctgtcatatc cgacatggcc ttccagaatc tcacgagctt ggagcgtctt attgtggacg 900  
 ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc accaagctca 960  
 aggaattttc aattgtacgt aattcgctgt cccacctcc tcccgatctc ccaggtaacg 1020  
 atctgatcag gctctatttg caggacaacc agataaacca cattcctttg acagccttct 1080  
 caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

```

aagggggttt tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200
tttgtgactg cagtattaaa tgggtcacag aatgggtcaa atatatccct tcatctctca 1260
acgtgcgggg tttcatgtgc caaggtcctg aacaagtccg ggggatggcc gtcaggggaat 1320
taaatatgaa tcttttgtcc tgtcccacca cgacccccgg cctgcctctc ttcaccccag 1380
ccccaagtac agcttctccg accactcagc ctcccaccct ctctattcca aaccctagca 1440
gaagctacac gcctccaact cctaccacat cgaaacttcc cacgattcct gactgggatg 1500
gcagagaaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560
atgatacttc cattcaagtc agctggctct ctctcttcac cgtgatggca taaaaactca 1620
catgggtgaa aatgggccac agtttagtag ggggcatcgt tcaggagcgc atagtcagcg 1680
gtgagaagca acacctgagc ctggttaact tagagccccg atccacctat cggatttgtt 1740
tagtgccact ggatgctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800
ccacccatgc ctctatctg aacaacggca gcaacacagc gtccagccat gagcagacga 1860
cgtcccacag catgggctcc ccttttctgc tggcgggctt gatcgggggc gcggtgatat 1920
ttgtgctggg ggtcttctc agcgtctttt gctggcatat gcacaaaaag gggcgctaca 1980
cctcccagaa gtggaaatac aaccggggcc ggcggaaga tgattattgc gaggcaggca 2040
ccaagaagga caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100
ataacgatca actccttaaa ggagatttca gactgcagcc catttacacc ccaaattggg 2160
gcattaatta cacagactgc catatcccca acaacatgcg atactgcaac agcagcgtgc 2220
cagacctgga gcactgcat acgtgacagc cagaggccca gcgttatcaa ggcggacaat 2280
tagactcttg agaacacact cgtgtgtgca cataaagaca cgcagattac atttgataaa 2340
tgttacacag atgcatttgc gcatttgaat actctgtaat ttatacgggtg tactatataa 2400
tgggatttaa aaaaagtgc atcttttcta tttcaagtta attacaaaca gttttgtaac 2460
tctttgcttt ttaaattctt

```

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

```

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
  1                      5                      10                      15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
          20                      25                      30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
          35                      40                      45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
          50                      55                      60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
          65                      70                      75                      80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
          85                      90                      95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
          100                      105                      110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
          115                      120                      125

```

Leu	Ala	Gln	Leu	Leu	Lys	Leu	Glu	Glu	Leu	His	Leu	Asp	Asp	Asn	Ser
130						135					140				
Ile	Ser	Thr	Val	Gly	Val	Glu	Asp	Gly	Ala	Phe	Arg	Glu	Ala	Ile	Ser
145					150					155					160
Leu	Lys	Leu	Leu	Phe	Leu	Ser	Lys	Asn	His	Leu	Ser	Ser	Val	Pro	Val
				165					170					175	
Gly	Leu	Pro	Val	Asp	Leu	Gln	Glu	Leu	Arg	Val	Asp	Glu	Asn	Arg	Ile
			180					185					190		
Ala	Val	Ile	Ser	Asp	Met	Ala	Phe	Gln	Asn	Leu	Thr	Ser	Leu	Glu	Arg
		195					200					205			
Leu	Ile	Val	Asp	Gly	Asn	Leu	Leu	Thr	Asn	Lys	Gly	Ile	Ala	Glu	Gly
	210					215					220				
Thr	Phe	Ser	His	Leu	Thr	Lys	Leu	Lys	Glu	Phe	Ser	Ile	Val	Arg	Asn
225					230					235					240
Ser	Leu	Ser	His	Pro	Pro	Pro	Asp	Leu	Pro	Gly	Thr	His	Leu	Ile	Arg
				245					250					255	
Leu	Tyr	Leu	Gln	Asp	Asn	Gln	Ile	Asn	His	Ile	Pro	Leu	Thr	Ala	Phe
			260					265					270		
Ser	Asn	Leu	Arg	Lys	Leu	Glu	Arg	Leu	Asp	Ile	Ser	Asn	Asn	Gln	Leu
		275					280					285			
Arg	Met	Leu	Thr	Gln	Gly	Val	Phe	Asp	Asn	Leu	Ser	Asn	Leu	Lys	Gln
	290					295					300				
Leu	Thr	Ala	Arg	Asn	Asn	Pro	Trp	Phe	Cys	Asp	Cys	Ser	Ile	Lys	Trp
305					310					315					320
Val	Thr	Glu	Trp	Leu	Lys	Tyr	Ile	Pro	Ser	Ser	Leu	Asn	Val	Arg	Gly
				325					330					335	
Phe	Met	Cys	Gln	Gly	Pro	Glu	Gln	Val	Arg	Gly	Met	Ala	Val	Arg	Glu
			340					345					350		
Leu	Asn	Met	Asn	Leu	Leu	Ser	Cys	Pro	Thr	Thr	Thr	Pro	Gly	Leu	Pro
		355					360					365			
Leu	Phe	Thr	Pro	Ala	Pro	Ser	Thr	Ala	Ser	Pro	Thr	Thr	Gln	Pro	Pro
	370					375					380				
Thr	Leu	Ser	Ile	Pro	Asn	Pro	Ser	Arg	Ser	Tyr	Thr	Pro	Pro	Thr	Pro
385					390					395					400
Thr	Thr	Ser	Lys	Leu	Pro	Thr	Ile	Pro	Asp	Trp	Asp	Gly	Arg	Glu	Arg

<210>	29
<211>	21
<212>	DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggtctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttgagca agcggcggcg gcggagacag aggcagaggc agaagctggg gctccgtcct 60  
cgctccac gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

gaggaagacc cgggtggctg cgccttccc agatgtctgc aggcgtgctt ctgctgatcc 180  
 tgccctctt gctcgccttg aaaatggaaa cctgcccagg ccaggagcgg gtcacgtggg aggtccatct 240  
 tgggacagat cgtcctcctc cctgcccagg ccaggagcgg gtcacgtggg aggtccatct 300  
 ctaggggagc acacgctcgg acccaccggc agacggccct tctggagagt tctgtgaga 360  
 acaagcgggc agacctgggt ttcattcatt acagctctcg cagtgtcaac acccatgact 420  
 atgcaaaggc caaggagttc atcgtggaca tcttgcaatt cttggacatt ggtcctgatg 480  
 tcacccgagt gggcctgctc caatatggca gcactgtcaa gaatgagttc tccctcaaga 540  
 ccttcaagag gaagtccgag gtggagcgtg ctgtcaagag gatgcggcat ctgtccacgg 600  
 gcacccatgac tgggctggcc atccagtatg ccctgaacat cgcattctca gaagcagagg 660  
 gggcccgccc cctgaggagg aatgtgccac gggtcataat gatcgtgaca gatgggagac 720  
 ctcaggactc cgtggccgag gtggctgcta aggcacggga cacgggcatc ctaattcttg 780  
 ccattggtgt gggccaggta gacttcaaca ccttgaagtc cattgggagt gagccccatg 840  
 aggaccatgt cttccttggt gccaatctca gccagattga gacgtgacc tccgtgttcc 900  
 agaagaagtt gtgcacggcc cacatgtgca gcaccctgga gcataactgt gccacttct 960  
 gcatcaacat ccctggctca tacgtctgca ggtgcaaaca aggctacatt ctcaactcgg 1020  
 atcagacgac ttgcagaatc caggatctgt gtgccatgga ggaccacaac tgtgagcagc 1080  
 tctgtgtgaa tgtgccgggc tccttcgtct gccagtgtca cagtggctac gccctggctg 1140  
 aggatgggaa gaggtgtgtg gctgtggact actgtgcctc agaaaaccac ggatgtgaac 1200  
 atgagtgtgt aaatgctgat ggctcctacc tttgccagtg ccatgaagga tttgctctta 1260  
 acccagatga aaaaacgtgc acaaggatca actactgtgc actgaacaaa cggggtgtg 1320  
 agcatgagtg cgtcaacatg gaggagagct actactgccg ctgccaccgt ggctacactc 1380  
 tggaccccaa tggcaaaacc tgcagccgag tggaccactg tgcacagcag gaccatggct 1440  
 gtgagcagct gtgtctgaac acggaggatt ccttcgtctg ccagtgtca gaaggcttcc 1500  
 tcatcaacga ggacctcaag acctgtcccc ggggtgatta ctgctgtctg agtgaccatg 1560  
 gttgtgaata ttcctgtgtc aacatggaca gatcctttgc ctgtcagtgt cctgagggac 1620  
 acgtgtccg cagcagtggt aagacgtgtg caaaattgga ctctgtgtct ctgggggacc 1680  
 acggtgtgtg acattcgtgt gtaagcagtg aagattcgtt tgtgtgccag tgctttgaag 1740  
 gttatatact ccgtgaagat ggaaaaacct gcagaaggaa agatgtctgc caagctatag 1800  
 accatggctg tgaacacatt tgtgtgaaca gtgacgactc atacacgtgc gagtgttgg 1860  
 agggattccg gctcgtgag gatgggaaac gctgccgaag gaaggatgtc tgcaaatcaa 1920  
 cccaccatgg ctgcgaacac atttgtgtta ataattggaa ttctacatc tgcaaatgct 1980  
 cagagggatt tgttctagct gaggacggaa gacggtgcaa gaaatgcact gaaggcccaa 2040  
 ttgacctggg ctttgtgatc gatggatcca agagtcttgg agaagagaat tttgaggctg 2100  
 tgaagcagtt tgtcactgga attatagatt ccttgacaat tcccccaaa gccgctcgag 2160  
 tggggtgtg cagtatctcc acacaggtcc acacagagtt cactctgaga aacttcaact 2220  
 cagccaaaga catgaaaaaa gccgtggccc acatgaaata catgggaaag ggtctatga 2280  
 ctgggctggc cctgaaacac atgtttgaga gaagttttac ccaaggagaa ggggcccagg 2340  
 ccctttccac aagggtgccc agagcagcca ttgtgttcac cgacggacgg gctcaggatg 2400  
 acgtctccga gtgggcccag aaagccaagg ccaatgggat cactatgtat gctgtgggg 2460  
 taggaaaagc cattgaggag gaactacaag agattgcctc tgagcccaca aacaagcatc 2520  
 tcttctatgc cgaagacttc agcacaatgg atgagataag tgaaaaactc aagaaaggca 2580  
 tctgtgaagc tctagaagac tccgatggaa gacaggactc tccagcaggg gaactgcaa 2640  
 aaacgggtcc acagccaaca gaatctgagc cagtcccat aaatatccaa gacctactt 2700  
 cctgttctaa ttttgagtg caacacagat atctgtttga agaagacaat cttttacgg 2760  
 ctacacaaaa gctttcccat tcaacaaaac cttcagggaag ccctttggaa gaaaaacacg 2820  
 atcaatgcaa atgtgaaaac cttataatgt tccagaacct tgcaaacgaa gaagtaagaa 2880  
 aattaacaca gcgcttagaa gaaatgacac agagaatgga agccctggaa aatgcctga 2940  
 gatacagatg aagattagaa atcgcgacac atttgtagtc attgtatcac ggattacaat 3000  
 gaacgcagtg cagagcccca aagctcaggc tattgttaaa tcaataatgt tgtgaagtaa 3060  
 aacaatcagt actgagaaac ctggtttgcc acagaacaaa gacaagaagt atacactaac 3120  
 ttgtataaat ttatctagga aaaaaatcct tcagaattct aagatgaatt taccaggtga 3180  
 gaatgaataa gctatgcaag gtattttgta atatactgtg gacacaactt gcttctgcct 3240  
 catcctgcct tagtgtgcaa tctcatttga ctatacgata aagtttgcac agtcttactt 3300



ctgtagaaca ctggccatag gaaatgctgt ttttttgtac tggactttac cttgatatat 3360  
 gtatatggat gtatgcataa aatcatagga catatgtact tgtggaacaa gttggatttt 3420  
 ttatacaata ttaaaattca ccacttcag 3449

<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile  
 1 5 10 15

Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile  
 20 25 30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
 85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
 130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
 145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
 195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

059020550

225		230		235		240
Met Cys Ser Thr	Leu Glu His Asn Cys	Ala His Phe Cys	Ile Asn Ile			
	245	250	255			
Pro Gly Ser Tyr	Val Cys Arg Cys	Lys Gln Gly Tyr	Ile Leu Asn Ser			
	260	265	270			
Asp Gln Thr Thr	Cys Arg Ile Gln Asp	Leu Cys Ala Met	Glu Asp His			
	275	280	285			
Asn Cys Glu Gln	Leu Cys Val Asn Val	Pro Gly Ser Phe	Val Cys Gln			
	290	295	300			
Cys Tyr Ser Gly	Tyr Ala Leu Ala	Glu Asp Gly Lys	Arg Cys Val Ala			
	305	310	315	320		
Val Asp Tyr Cys	Ala Ser Glu Asn His	Gly Cys Glu His	Glu Cys Val			
	325	330	335			
Asn Ala Asp Gly	Ser Tyr Leu Cys	Gln Cys His Glu	Gly Phe Ala Leu			
	340	345	350			
Asn Pro Asp Glu	Lys Thr Cys Thr	Arg Ile Asn Tyr	Cys Ala Leu Asn			
	355	360	365			
Lys Pro Gly Cys	Glu His Glu Cys	Val Asn Met Glu	Glu Ser Tyr Tyr			
	370	375	380			
Cys Arg Cys His	Arg Gly Tyr Thr	Leu Asp Pro Asn	Gly Lys Thr Cys			
	385	390	395	400		
Ser Arg Val Asp	His Cys Ala Gln	Gln Asp His Gly	Cys Glu Gln Leu			
	405	410	415			
Cys Leu Asn Thr	Glu Asp Ser Phe	Val Cys Gln Cys	Ser Glu Gly Phe			
	420	425	430			
Leu Ile Asn Glu	Asp Leu Lys Thr	Cys Ser Arg Val	Asp Tyr Cys Leu			
	435	440	445			
Leu Ser Asp His	Gly Cys Glu Tyr	Ser Cys Val Asn	Met Asp Arg Ser			
	450	455	460			
Phe Ala Cys Gln	Cys Pro Glu Gly	His Val Leu Arg	Ser Asp Gly Lys			
	465	470	475	480		
Thr Cys Ala Lys	Leu Asp Ser Cys	Ala Leu Gly Asp	His Gly Cys Glu			
	485	490	495			
His Ser Cys Val	Ser Ser Glu Asp	Ser Phe Val Cys	Gln Cys Phe Glu			
	500	505	510			

09002615.071004

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
 515 520 525  
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540  
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560  
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575  
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
 580 585 590  
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
 595 600 605  
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620  
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
 625 630 635 640  
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
 645 650 655  
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670  
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685  
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
 690 695 700  
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
 705 710 715 720  
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
 725 730 735  
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
 740 745 750  
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765  
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
 770 775 780  
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
900 905 910

Arg Tyr Arg  
915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 37

gcctgtcagt gtcttgaggg acacgtgctc cgcagc gatg ggaag

45

&lt;210&gt; 38

&lt;211&gt; 1813

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

```

ggagccgccc tgggtgtcag cggctcggct cccgcgcacg ctccggccgt cgcgcagcct 60
cggcacctgc aggtccgtgc gtcccgcggc tggcgcgccct gaactccgtcc cggccagggg 120
gggccatgat ttccctcccg gggccctcgg tgaccaaactt gctgcgggttt ttgttccttg 180
ggctgagtgc cctcgcgccc cctcgcggg cccagctgca actgcacttg cccgccaaacc 240
ggttgcaggc ggtggaggga ggggaagtgg tgcttccagc gtggtacacc ttgcacgggg 300
aggtgtcttc atcccagcca tgggaggtgc cctttgtgat gtggttcttc aaacagaaag 360
aaaaggagga tcaggtgttg tcctacatca atggggtcac aacaagcaaa cctggagtat 420
ccttggtcta ctccatgccc tcccgaacc tgtccctgcg gctggagggt ctccaggaga 480
aagactctgg cccctacagc tgctccgtga atgtgcaaga caaacaaggc aaatctaggg 540
gccacagcat caaaacctta gaactcaatg tactggttcc tccagctcct ccactctgcc 600
gtctccaggg tgtgccccat gtgggggcaa acgtgaccct gagctgccag tctccaagga 660
gtaagcccg cgtccaatac cagtgggatc ggcagcttcc atccttccag actttctttg 720
caccagcatt agatgtcatc cgtgggtctt taagcctcac caacctttcg tcttccatgg 780
ctggagtcta tgtctgcaag gccacacaatg aggtgggcac tgcccaatgt aatgtgacgc 840
tggaagtgag cacaggccct ggagctgcag tgggtgctgg agctgttggtg ggtaccctgg 900
ttggactggg gttgctggct gggctggctc tcttgtaacca ccgccggggc aaggccctgg 960
aggagccagc caatgatatc aaggaggatg ccattgctcc ccggaccctg ccttgggcca 1020
agagctcaga cacaatctcc aagaatggga ccctttcctc tgtcacctcc gcacgagccc 1080
tccggccacc ccatggccct cccaggcctg gtgcattgac ccccacgccc agtctctcca 1140
gccaggccct gccctcacca agactgccc cgcagatgg ggcccaccct caaccaatat 1200
cccccatccc tgggtggggt tcttcctctg gcttgagccg catgggtgct gtgctgtga 1260
tggtgcctgc ccagagtcaa gctggctctc tggatatgatg accccaccac tcattggcta 1320
aaggatttgg ggtctctcct tcctataagg gtcacctcta gcacagaggc ctgagtcattg 1380
ggaaagagtc acactcctga cccttagtac tctgccccca cctctcttta ctgtgggaaa 1440
accatctcag taagacctaa gtgtccagga gacagaagga gaagaggaag tggatctgga 1500
attgggagga gcctccaccc acccctgact cctccttatg aagccagctg ctgaaattag 1560
ctactacca agagtgaggg gcagagactt ccagtcactg agtctcccag gcccccttga 1620
tctgtacccc acccctatct aacaccaccc ttggctccca ctccagctcc ctgtattgat 1680
ataacctgtc aggctggctt ggtaggttt tactggggca gaggataggg aatctcttat 1740
taaaactaac atgaaatatg tgttgttttc atttgcaaat ttaaataaag atacataatg 1800
tttgtatgaa aaa 1813

```

&lt;210&gt; 39

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15												
Phe	Leu	Gly	Leu	Ser	Ala	Leu	Ala	Pro	Pro	Ser	Arg	Ala	Gln	Leu	Gln
			20					25					30		
Leu	His	Leu	Pro	Ala	Asn	Arg	Leu	Gln	Ala	Val	Glu	Gly	Gly	Glu	Val
		35					40					45			
Val	Leu	Pro	Ala	Trp	Tyr	Thr	Leu	His	Gly	Glu	Val	Ser	Ser	Ser	Gln
	50					55					60				
Pro	Trp	Glu	Val	Pro	Phe	Val	Met	Trp	Phe	Phe	Lys	Gln	Lys	Glu	Lys
	65				70					75					80
Glu	Asp	Gln	Val	Leu	Ser	Tyr	Ile	Asn	Gly	Val	Thr	Thr	Ser	Lys	Pro
				85					90					95	
Gly	Val	Ser	Leu	Val	Tyr	Ser	Met	Pro	Ser	Arg	Asn	Leu	Ser	Leu	Arg
			100					105					110		
Leu	Glu	Gly	Leu	Gln	Glu	Lys	Asp	Ser	Gly	Pro	Tyr	Ser	Cys	Ser	Val
		115					120					125			
Asn	Val	Gln	Asp	Lys	Gln	Gly	Lys	Ser	Arg	Gly	His	Ser	Ile	Lys	Thr
	130					135					140				
Leu	Glu	Leu	Asn	Val	Leu	Val	Pro	Pro	Ala	Pro	Pro	Ser	Cys	Arg	Leu
	145				150					155					160
Gln	Gly	Val	Pro	His	Val	Gly	Ala	Asn	Val	Thr	Leu	Ser	Cys	Gln	Ser
				165					170					175	
Pro	Arg	Ser	Lys	Pro	Ala	Val	Gln	Tyr	Gln	Trp	Asp	Arg	Gln	Leu	Pro
			180					185					190		
Ser	Phe	Gln	Thr	Phe	Phe	Ala	Pro	Ala	Leu	Asp	Val	Ile	Arg	Gly	Ser
		195					200					205			
Leu	Ser	Leu	Thr	Asn	Leu	Ser	Ser	Ser	Met	Ala	Gly	Val	Tyr	Val	Cys
		210				215					220				
Lys	Ala	His	Asn	Glu	Val	Gly	Thr	Ala	Gln	Cys	Asn	Val	Thr	Leu	Glu
	225				230					235					240
Val	Ser	Thr	Gly	Pro	Gly	Ala	Ala	Val	Val	Ala	Gly	Ala	Val	Val	Gly
				245					250					255	
Thr	Leu	Val	Gly	Leu	Gly	Leu	Leu	Ala	Gly	Leu	Val	Leu	Leu	Tyr	His
			260					265						270	
Arg	Arg	Gly	Lys	Ala	Leu	Glu	Glu	Pro	Ala	Asn	Asp	Ile	Lys	Glu	Asp
			275				280					285			

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 42  
 ggccacagca tcaaaacctt agaactcaat gtactgggtc ctccagctcc 50  
  
 <210> 43  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 43  
 gtgtgacaca gcgtgggc 18  
  
 <210> 44  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 44  
 gaccggcagg cttctgcg 18  
  
 <210> 45  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 45  
 cagcagcttc agccaccagg agtgg 25  
  
 <210> 46  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 46  
 ctgagccgtg ggctgcagtc tcgc 24  
  
 <210> 47



<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 47  
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48  
 <211> 2822  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
 cgccaccact gcggccaccg ccaatgaaac gcctcccgt cctagtgggt tttccactt 60  
 tgttgaattg ttcctatact caaaattgca ccaagacacc ttgtctccca aatgcaaaat 120  
 gtgaaatcac caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180  
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtccctgt ggcgaaaatg 240  
 ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300  
 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360  
 caaactgcc a ttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420  
 tcagatccat aaaagaacct gtggccttgc tacaagaagt ctatagaaat tctgtgacag 480  
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540  
 taggttacaa gaacaacact atctcagcca aggacaccct ttctaactca actcttactg 600  
 aattttgtaa aaccgtgaat aattttgttc aaaagggtac atttgtagtt tgggacaagt 660  
 tatctgtgaa tcataggaga acacatctta caaaactcat gcacactgtt gaacaagcta 720  
 ctttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780  
 tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840  
 atatggatgg agactacata aatatatttc caaagagaaa agctgcatat gattcaaatg 900  
 gcaattgtgc agttgcattt ttatattata agagtattgg tcttttgctt tcatcatctg 960  
 acaacttctt attgaaacct caaaattatg ataattctga agaggaggaa agagtcatat 1020  
 cttcagtaatt ttcagctca atgagctcaa acccaccac attatatgaa cttgaaaaaa 1080  
 taacatttac attaatgcat cgaaagggtc cagataggta taggagtcta tgtgcatttt 1140  
 ggaattactc acctgatacc atgaatggca gctgggtctt agagggctgt gagctgacat 1200  
 actcaaatga gaccacacc tcatgccgt gtaatcacct gacacatttt gcaattttga 1260  
 tgtcctctgg tcttccatt ggtattaaag attataatat tcttacaagg atcactcaac 1320  
 taggaataat tatttctactg atttgtcttg ccatatgcat ttttaccttc tgggtcttca 1380  
 gtgaaattca aagcaccagg acaacaattc acaaaaatct ttgctgtagc ctatttcttg 1440  
 ctgaacttgt ttttcttggt gggatcaata caaatactaa taagctcttc tgttcaatca 1500  
 ttgccggact gctacactac ttcttttttag ctgcttttgc atggatgtgc attgaaggca 1560  
 tacatctcta tctcattggt gtgggtgtca tctacaacaa gggatttttg cacaagaatt 1620  
 tttatatctt tggctatcta agcccagccg tggtagttgg attttcggca gcactaggat 1680  
 acagatatta tggcacaacc aaagtatgtt ggcttagcac cgaaaaaac tttatttgga 1740  
 gttttatagg accagcatgc ctaatcattc ttgttaatct cttggctttt ggagtcacat 1800  
 tatacaaatg ttttcgtcac actgcagggt tgaaaccaga agttagttgc tttgagaaca 1860  
 taaggtcttg tgcaagagga gccctcgctc ttctgttctt tctcggcacc acctggatct 1920  
 ttgggttctt cctggttggt cacgcacatc ttggttacagc ttacctcttc acagtcagca 1980  
 atgttttcca ggggatgttc atttttttat tctgtgtgt tttatctaga aagattcaag 2040  
 aagaatatta cagattgttc aaaaatgtcc cctgttgttt tggatgttta aggtaaacat 2100  
 agagaatggg ggataattac aactgcacaa aaataaaaat tccaagctgt ggatgaccaa 2160

```

tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaa agtatttttaa 2220
atcagttttt ctgtttatgc tataggaact gtagataata aggtaaaatt atgtatcata 2280
tagatatact atgtttttct atgtgaaata gttctgtcaa aaatagtatt gcagatattt 2340
ggaaagtaat tggttttctca ggagtgatat cactgcaccc aaggaaagat tttctttcta 2400
acacgagaag tatatgaatg tcttgaagga aaccactggc ttgatatttc tgtgactcgt 2460
gttgcccttg aaactagtcc cctaccacct cggtaatgag ctccattaca gaaagtggaa 2520
cataagagaa tgaaggggca gaatatcaaa cagtgaaaag ggaatgataa gatgtatttt 2580
gaatgaactg ttttttctgt agactagctg agaaattggt gacataaaat aaagaattga 2640
agaaacacat tttaccattt tgtgaattgt tctgaactta aatgtccact aaaacaactt 2700
agacttctgt ttgctaaatc tgtttctttt tctaatttc taaaaaaaaa aaaaagggtt 2760
acctccacaa attgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2820
aa 2822

```

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

```

Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
  1                      5                      10                      15

```

```

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
          20                      25                      30

```

```

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
          35                      40                      45

```

```

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
          50                      55                      60

```

```

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
          65                      70                      75                      80

```

```

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
          85                      90                      95

```

```

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
          100                      105                      110

```

```

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
          115                      120                      125

```

```

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
          130                      135                      140

```

```

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
          145                      150                      155                      160

```

```

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
          165                      170                      175

```

```

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

```

09903615.01001

			180				185				190					
Glu	Phe	Val	Lys	Thr	Val	Asn	Asn	Phe	Val	Gln	Arg	Asp	Thr	Phe	Val	
			195				200				205					
Val	Trp	Asp	Lys	Leu	Ser	Val	Asn	His	Arg	Arg	Thr	His	Leu	Thr	Lys	
			210				215				220					
Leu	Met	His	Thr	Val	Glu	Gln	Ala	Thr	Leu	Arg	Ile	Ser	Gln	Ser	Phe	
			225				230				235				240	
Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys	
			245				250				255					
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met	
			260				265				270					
Asn	Met	Asp	Gly	Asp	Tyr	Ile	Asn	Ile	Phe	Pro	Lys	Arg	Lys	Ala	Ala	
			275				280				285					
Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser	
			290				295				300					
Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln	
			305				310				315				320	
Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile	
			325				330				335					
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys	
			340				345				350					
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser	
			355				360				365					
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp	
			370				375				380					
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser	
			385				390				395				400	
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly	
			405				410				415					
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln	
			420				425				430					
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr	
			435				440				445					
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys	
			450				455				460					

```
<220>  
<221> modified_base  
<222> (61)
```

<400> 50						
tggaaacata	tcttcctca	tatgaatatg	gatggagact	acataaatat	atttccaaag	60
ngaaaagccg	gcatatggat	tcaaattggca	atgttgca	tgcattttta	tattataaga	120
gtattggtcc	ctttgctttc	atcatctgac	aacttcttat	tgaacctca	aaattatgat	180
aattctgaag	aggaggaaag	agtcatatct	tcagtaattt	cagtctcaat	gagctcaaac	240
ccaccacat	tatatgaact	tgaaaaaata	acatttacat	taagtcacat	aaaggtcaca	300
gataggatata	ggagtctatg	tggcattttg	gaatactcac	ctgataccat	gaatggcagc	360
tggctctcag	agggtcttga	gctgacatac	tcaaattgaga	cccacacctc	atgccgctgt	420
aatcacctga	cacattttgc	aattttgatg	tctcttggtc	tttccatttg	tattaaagat	480
tataatattc	ttacaaggat	cactcaacta	ggaataatta	tttccactgat	ttgtcttgcc	540
atatgcattt	ttaccttctg	gttcttcagt	gaaattcaaa	gcaccagga		589

<211> 20

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

gqtaatgagc tccattacag 20

<211> 18

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

ggagtagaaa gcgcatgg 18

<211> 22

### <213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

cacctgatac catgaatggc ag 22

<211> 18

<212> DNA

$\langle 220 \rangle$ 

<400> 54

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<400> 55

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<400> 56

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<400> 57

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60  
cgctaagcga ggcctcctcc tccgcagat ccgaacggcc tgggcggggt cccccggct 120

gggacaagaa gccgccgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180  
 aggcgggggtg tgagtgggtg tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa 240  
 tgctcgggtg tcttgggcac ctaccctgtg ggcccgtaag gcgctactat ataaggctgc 300  
 cggcccggag ccgcgcgcgc gtcagagcag gagcgcctgcg tccaggatct agggccacga 360  
 ccatcccaac ccggcactca cagccccgca gcgcatcccg gtcgcgcgcc agcctccgcg 420  
 acccccatcg ccggagctgc gccgagagcc ccaggagggt gccatgcgga gcggtgtgtg 480  
 ggtggtccac gtatggatcc tggccggcct ctggctggcc gtggccgggc gccccctcgc 540  
 cttctcggac gcggggcccc acgtgcacta cggctggggc gaccccatcc gcctgcggca 600  
 cctgtacacc tccggcccc acgggctctc cagctgcttc ctgcgcaccc gtgccgacgg 660  
 cgtcgtggac tgccgcggg gccagagcgc gcacagtttg ctggagatca aggcagtcgc 720  
 tctgcggacc gtggccatca agggcgtgca cagcgtgcgg tacctctgca tgggcgcgca 780  
 cggcaagatg caggggctgc ttcagtactc ggaggaagac tgtgctttcg aggaggagat 840  
 ccgcccagat ggctacaatg tgtaccgatc cgagaagcac cgcctcccgg tctccctgag 900  
 cagtgcacaa cagcggcagc tgtacaagaa cagaggcttt cttccactct ctcatttcct 960  
 gcccatgctg cccatggtcc cagaggagcc tgaggacctc agggggccact tggaatctga 1020  
 catgttctct tcgcccctgg agaccgacag catggaccga tttgggcttg tcaccggact 1080  
 ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatgcccgg gcctcttcac 1140  
 tgctgccagg ggctgtggtt cctgcagcgt gggggacgtg cttctacaag aacagtcctg 1200  
 agtccacgtt ctgtttagct ttaggaagaa acatctagaa gttgtacata ttcagagttt 1260  
 tccattggca gtgccagttt ctagccaata gacttgctg atcataacat tgtaagcctg 1320  
 tagcttgccc agctgctgcc tgggccccca ttctgctccc tcgaggttgc tggacaagct 1380  
 gctgcactgt ctcagttctg cttgaatacc tccatcgatg gggaaactcac ttcctttgga 1440  
 aaaattctta tgtcaagctg aaattctcta attttttctc atcaactccc caggagcagc 1500  
 cagaagacag gcagtagttt taatttcagg aacagggtgat ccaactctgta aaacagcagg 1560  
 taaatttcac tcaaccccat gtgggaattg atctatatct ctacttccag ggaccatttg 1620  
 cccttcccaa atccctccag gccagaactg actggagcag gcatggccca ccaggcttca 1680  
 ggagtagggg aagcctggag cccactcca gccctgggac aacttgagaa tccccctga 1740  
 ggccagttct gtcatggatg ctgtcctgag aataaactgc tgtcccgggtg tcacctgctt 1800  
 ccatctccca gccaccagc cctctgcca cctcacatgc ctccccatgg attggggcct 1860  
 cccaggcccc ccaccttatg tcaacctgca cttcttgctt aaaaatcagg aaaagaaaag 1920  
 atttgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagacctt 1980  
 gaaccctttc cccagcactt ggttttccaa catgatattt atgagtaatt tattttgata 2040  
 tgtacatctc ttattttctt acattattta tgccccaaa ttatatttat gtatgtaagt 2100  
 gaggtttggt ttgtatatta aaatggagtt tgtttgt 2137

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu  
 1 5 10 15

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
 50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80  
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95  
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110  
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125  
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140  
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160  
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175  
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190  
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205  
 Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

&lt;210&gt; 60

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 60

atccgcccag atggctacaa tgtgta

26

&lt;210&gt; 61

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 61

gcctccccgt ctccctgagc agtgccaaac agcggcagtg ta

42

T00120 "CTGCGG"



<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtccggt gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60  
 cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120  
 gctgctgctg cgctacctgg tggtcgccct gggctatcat aaggcctatg ggttttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctatatt tagcctgcaa 240  
 aaccccaaag aagactgttt cctccagatt agagtggag aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360  
 tttcaatatc cggatcaaaa atgtgacaag aagtgatgcg gggaaatatc gtttgtgaagt 420  
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tgggaagtatt 480  
 agtggtccca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggg 540  
 agagctacga tgtcaagaca aagaagggaa tccagctcct gaatacacat ggtttaagga 600  
 tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660  
 aatgaatata aaaactggaa ctctgcaatt taatactgtt tccaaactgg aactggaga 720  
 atattcctgt gaagcccgcga attctgttgg atatcgagg tgcctggga aacgaatgca 780  
 agtagatgat ctcaacataa gtggcatcat agcagccgta gtagttgtgg ccttagtgat 840  
 ttccgtttgt ggcttgggtg tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900  
 ctccctccag aagagtaatt cttcatctaa agccacgaca atgagtgaat atgtgcagt 960  
 gctcacgcct gtaatcccag cactttggaa ggcgcggcg ggcggatcac gaggtcagga 1020  
 gttctagacc agtctggcca atatggtgaa acccatctc tactaaaata caaaaattag 1080  
 ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140  
 acccgggagg cggaggttgc agtgagctga gatcacgcca ctgcagtcca gcctgggtaa 1200  
 cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact ggtttttacc 1260  
 tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 1 5 10 15  
 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

Lys	Asp	Gln	Gln	Val	Val	Thr	Ala	Val	Glu	Tyr	Gln	Glu	Ala	Ile	Leu
35						40						45			
Ala	Cys	Lys	Thr	Pro	Lys	Lys	Thr	Val	Ser	Ser	Arg	Leu	Glu	Trp	Lys
50						55				60					
Lys	Leu	Gly	Arg	Ser	Val	Ser	Phe	Val	Tyr	Tyr	Gln	Gln	Thr	Leu	Gln
65				70				75						80	
Gly	Asp	Phe	Lys	Asn	Arg	Ala	Glu	Met	Ile	Asp	Phe	Asn	Ile	Arg	Ile
				85				90						95	
Lys	Asn	Val	Thr	Arg	Ser	Asp	Ala	Gly	Lys	Tyr	Arg	Cys	Glu	Val	Ser
		100						105				110			
Ala	Pro	Ser	Glu	Gln	Gly	Gln	Asn	Leu	Glu	Glu	Asp	Thr	Val	Thr	Leu
115						120						125			
Glu	Val	Leu	Val	Ala	Pro	Ala	Val	Pro	Ser	Cys	Glu	Val	Pro	Ser	Ser
130						135				140					
Ala	Leu	Ser	Gly	Thr	Val	Val	Glu	Leu	Arg	Cys	Gln	Asp	Lys	Glu	Gly
145				150						155				160	
Asn	Pro	Ala	Pro	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Arg	Leu	Leu
				165				170						175	
Glu	Asn	Pro	Arg	Leu	Gly	Ser	Gln	Ser	Thr	Asn	Ser	Ser	Tyr	Thr	Met
		180						185				190			
Asn	Thr	Lys	Thr	Gly	Thr	Leu	Gln	Phe	Asn	Thr	Val	Ser	Lys	Leu	Asp
195						200						205			
Thr	Gly	Glu	Tyr	Ser	Cys	Glu	Ala	Arg	Asn	Ser	Val	Gly	Tyr	Arg	Arg
210						215				220					
Cys	Pro	Gly	Lys	Arg	Met	Gln	Val	Asp	Asp	Leu	Asn	Ile	Ser	Gly	Ile
225				230						235				240	
Ile	Ala	Ala	Val	Val	Val	Val	Ala	Leu	Val	Ile	Ser	Val	Cys	Gly	Leu
				245				250						255	
Gly	Val	Cys	Tyr	Ala	Gln	Arg	Lys	Gly	Tyr	Phe	Ser	Lys	Glu	Thr	Ser
		260						265				270			
Phe	Gln	Lys	Ser	Asn	Ser	Ser	Ser	Lys	Ala	Thr	Thr	Met	Ser	Glu	Asn
275						280						285			
Val	Gln	Trp	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Lys	Ala	Ala	Ala
290						295				300					
Gly	Gly	Ser	Arg	Gly	Gln	Glu	Phe								

310

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

```
<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence
```

```
<400> 66
acctgcgata tccaacagaa ttg                23
```

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 67  
ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

```
<210> 68
<211> 2639
<212> DNA
<213> Homo sapiens
```

<400> 68							
gacatcggag	gtgggctagc	actgaaactg	cttttcaaga	cgaggaagag	gaggagaaaag		60
agaaagaaga	ggaagatggt	gggcaacatt	tattttaacat	gctccacagc	cgggaccttg		120
gcatcatgct	gctattcctg	caaatactga	agaagcatgg	gatttaaata	ttttacttct		180
aaataaatga	attactcaat	ctcctatgac	catctataca	tactccacct	tcaaaaagta		240
catcaatatt	atatcattaa	ggaaatagta	accttctctt	ctccaatatg	catgacattt		300
ttggacaatg	caattgtggc	actggcactt	atttcagtga	agaaaaactt	tgtggttcta		360
tggcattcat	catttgacaa	atgcaagcat	cttccttatc	aatcagctcc	tattgaactt		420
actagcactg	actgtggaat	ccctaagggc	ccattacatt	tctgaaagag	aaagctaaga		480
tgaaggacat	gccactccga	attcatgtgc	tacttggcct	agctatcact	acactagtac		540

aagctgtaga taaaaaagtg gattgtccac gggtatgtac gtgtgaaatc aggccttggt 600  
ttacacccag atccatttat atggaagcat ctacagtggg ttgtaatgat ttaggtcttt 660  
taactttccc agccagattg ccagctaaca cacagattct tctctacag actaacaata 720  
ttgcaaaaat tgaatactcc acagactttc cagtaaacct tactggcctg gatttatctc 780  
aaaacaatth atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctctttctcg 840  
tgtacctaga ggaaaacaaa cttactgaac tgctgaaaa atgtctgtcc gaactgagca 900  
acttacaaga actctatatt aatcacaact tgctttctac aatttcacct ggagccttta 960  
ttggcctaca taatcttctt cgacttcac tcaattcaaa tagattgcag atgatcaaca 1020  
gtaagtgggt tgatgctctt ccaaacttag agattctgat gattggggaa aatccaatta 1080  
tcagaatcaa agacatgaac ttaagcctc ttatcaatct tcgcagcctg gttatagctg 1140  
gtataaacct cacagaaata ccagataacg ccttggttgg actggaaaac ttagaaagca 1200  
tctcttttta cgataacagg cttattaaag taccatgt tgctcttcaa aaagttgtaa 1260  
atctcaaatt tttggatcta aataaaaaat ctattaatag aatacgaagg ggtgatttta 1320  
gcaatatgct acacttaaaa gagttgggga taaataatat gcctgagctg atttccatcg 1380  
atagtcttgc tgtggataac ctgccagatt taagaaaaat agaagctact aacaacccta 1440  
gattgtctta cattcacccc aatgcatttt tcagactccc caagctggaa tcaactcatg 1500  
tgaacagcaa tgctctcagt gccctgtacc atgggtaccat tgagtctctg ccaaacctca 1560  
aggaaatcag catacacagt aaccccatca ggtgtgactg tgtcatccgt tggatgaaca 1620  
tgaacaaaac caacattcga ttcattggagc cagattcact gttttgcgtg gacccacctg 1680  
aatccaagg tcagaatggt cggcaagtgc atttcaggga catgatggaa atttgtctcc 1740  
ctcttatagc tcttgagagc tttccttcta atctaaatgt agaagctggg agctatgttt 1800  
cctttcactg tagagctact gcagaaccac agcctgaaat ctactggata acaccttctg 1860  
gtcaaaaact cttgcctaact accctgacag acaagttcta tgtccattct gaggggaacac 1920  
tagatataaa tggcgtaact cccaaagaag ggggtttata tacttgtata gcaactaacc 1980  
tagttggcgc tgacttgaag tctgttatga tcaaagtggg tggatctttt ccacaagata 2040  
acaatggctc tttgaatatt aaaataagag atattcaggc caattcagtt ttggtgtcct 2100  
ggaaagcaag ttctaaaatt ctcaaactca gtgttaaagt gacagccttt gtcaagactg 2160  
aaaattctca tgctgcgcaa agtgctcgaa taccatctga tgtcaaggta tataatctta 2220  
ctcatctgaa tccatcaact gagtataaaa tttgtattga tattcccacc atctatcaga 2280  
aaaacagaaa aaaatgtgta aatgtcacca ccaaaggttt gcacctgat caaaaagagt 2340  
atgaaaagaa taataccaca acacttatgg cctgtcttgg aggccttctg gggattattg 2400  
gtgtgatatg tcttatcagc tgctctctc cagaaatgaa ctgtgatggg ggacacagct 2460  
atgtgaggaa ttacttacag aaaccaacct ttgcattagg tgagctttat cctcctctga 2520  
taaactctctg ggaagcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580  
taggtttacc aacaaatatg tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile  
1 5 10 15

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu  
20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
50 55 60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80  
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140  
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190  
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300  
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320  
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

0902646-04004  
 T00T405T00650

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
	405	410
		415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
	420	425
		430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
	435	440
		445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
		480
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
	485	490
		495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
	500	505
		510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
	515	520
		525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
		560
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
	565	570
		575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
	580	585
		590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

090615 07001

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

```

gccccgggact ggcgcaaggt gcccaagcaa ggaaagaaat aatgaagaga cacatgtgtt 60
agctgcagcc ttttgaaaca cgcaagaagg aaatcaatag tgtggacagg gctggaacct 120
ttaccacgct tgttgagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180
gaatctggta gacctgtggt taaccctgtc cctctccatg tgtctcctcc tacaaagttt 240
tgttcttatg atactgtgct ttcatctctgc cagtatgtgt cccaagggct gtctttgttc 300
ttcctctggg ggtttaaatg tcacctgtag caatgcaaat ctcaaggaaa tacctagaga 360
tcttctcct gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420
tgaaattttt aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgct 540
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600
aattgccaac aaccctggc actgcgactg tactctacag caagttctga ggagcatggc 660
gtccaatcat gagacagccc acaacgtgat ctgtaaaacg tccgtgttgg atgaacatgc 720
tggcagacca ttcctcaatg ctgccaaacga cgctgacctt tgtaacctcc ctaaaaaaac 780
taccgattat gccatgctgg tcacctgtt tggctgggtc actatggtga tctcatatgt 840
ggtatattat gtgaggcaaa atcaggagga tgcccggaga cacctcgaat acttgaaatc 900
cctgccaaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatagt 960
tccaaactga ctgtcattga gaaagaaaga aagtagtttg cgattgcagt agaaataagt 1020
ggtttacttc tcccatccat tgtaaacatt tgaaactttg tatttcagtt ttttttgaat 1080
tatgccactg ctgaaactttt aacaaacact acaacataaa taatttgagt ttaggtgatc 1140
cacccttaa ttgtaccccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200
tagatccatc tcactattta ataatgaaat ttattttttt aattttaaaag caaataaaaag 1260
cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

```

<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
 1 5 10 15  
 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290

03902345 04001  
 041001 042001  
 043001 044001  
 045001 046001  
 047001 048001  
 049001 050001  
 051001 052001  
 053001 054001  
 055001 056001  
 057001 058001  
 059001 060001  
 061001 062001  
 063001 064001  
 065001 066001  
 067001 068001  
 069001 070001  
 071001 072001  
 073001 074001  
 075001 076001  
 077001 078001  
 079001 080001  
 081001 082001  
 083001 084001  
 085001 086001  
 087001 088001  
 089001 090001  
 091001 092001  
 093001 094001  
 095001 096001  
 097001 098001  
 099001 100001  
 101001 102001  
 103001 104001  
 105001 106001  
 107001 108001  
 109001 110001  
 111001 112001  
 113001 114001  
 115001 116001  
 117001 118001  
 119001 120001  
 121001 122001  
 123001 124001  
 125001 126001  
 127001 128001  
 129001 130001  
 131001 132001  
 133001 134001  
 135001 136001  
 137001 138001  
 139001 140001  
 141001 142001  
 143001 144001  
 145001 146001  
 147001 148001  
 149001 150001  
 151001 152001  
 153001 154001  
 155001 156001  
 157001 158001  
 159001 160001  
 161001 162001  
 163001 164001  
 165001 166001  
 167001 168001  
 169001 170001  
 171001 172001  
 173001 174001  
 175001 176001  
 177001 178001  
 179001 180001  
 181001 182001  
 183001 184001  
 185001 186001  
 187001 188001  
 189001 190001  
 191001 192001  
 193001 194001  
 195001 196001  
 197001 198001  
 199001 200001  
 201001 202001  
 203001 204001  
 205001 206001  
 207001 208001  
 209001 210001  
 211001 212001  
 213001 214001  
 215001 216001  
 217001 218001  
 219001 220001  
 221001 222001  
 223001 224001  
 225001 226001  
 227001 228001  
 229001 230001  
 231001 232001  
 233001 234001  
 235001 236001  
 237001 238001  
 239001 240001  
 241001 242001  
 243001 244001  
 245001 246001  
 247001 248001  
 249001 250001  
 251001 252001  
 253001 254001  
 255001 256001  
 257001 258001  
 259001 260001  
 261001 262001  
 263001 264001  
 265001 266001  
 267001 268001  
 269001 270001  
 271001 272001  
 273001 274001  
 275001 276001  
 277001 278001  
 279001 280001  
 281001 282001  
 283001 284001  
 285001 286001  
 287001 288001  
 289001 290001  
 291001 292001  
 293001 294001  
 295001 296001  
 297001 298001  
 299001 300001  
 301001 302001  
 303001 304001  
 305001 306001  
 307001 308001  
 309001 310001  
 311001 312001  
 313001 314001  
 315001 316001  
 317001 318001  
 319001 320001  
 321001 322001  
 323001 324001  
 325001 326001  
 327001 328001  
 329001 330001  
 331001 332001  
 333001 334001  
 335001 336001  
 337001 338001  
 339001 340001  
 341001 342001  
 343001 344001  
 345001 346001  
 347001 348001  
 349001 350001  
 351001 352001  
 353001 354001  
 355001 356001  
 357001 358001  
 359001 360001  
 361001 362001  
 363001 364001  
 365001 366001  
 367001 368001  
 369001 370001  
 371001 372001  
 373001 374001  
 375001 376001  
 377001 378001  
 379001 380001  
 381001 382001  
 383001 384001  
 385001 386001  
 387001 388001  
 389001 390001  
 391001 392001  
 393001 394001  
 395001 396001  
 397001 398001  
 399001 400001  
 401001 402001  
 403001 404001  
 405001 406001  
 407001 408001  
 409001 410001  
 411001 412001  
 413001 414001  
 415001 416001  
 417001 418001  
 419001 420001  
 421001 422001  
 423001 424001  
 425001 426001  
 427001 428001  
 429001 430001  
 431001 432001  
 433001 434001  
 435001 436001  
 437001 438001  
 439001 440001  
 441001 442001  
 443001 444001  
 445001 446001  
 447001 448001  
 449001 450001  
 451001 452001  
 453001 454001  
 455001 456001  
 457001 458001  
 459001 460001  
 461001 462001  
 463001 464001  
 465001 466001  
 467001 468001  
 469001 470001  
 471001 472001  
 473001 474001  
 475001 476001  
 477001 478001  
 479001 480001  
 481001 482001  
 483001 484001  
 485001 486001  
 487001 488001  
 489001 490001  
 491001 492001  
 493001 494001  
 495001 496001  
 497001 498001  
 499001 500001  
 501001 502001  
 503001 504001  
 505001 506001  
 507001 508001  
 509001 510001  
 511001 512001  
 513001 514001  
 515001 516001  
 517001 518001  
 519001 520001  
 521001 522001  
 523001 524001  
 525001 526001  
 527001 528001  
 529001 530001  
 531001 532001  
 533001 534001  
 535001 536001  
 537001 538001  
 539001 540001  
 541001 542001  
 543001 544001  
 545001 546001  
 547001 548001  
 549001 550001  
 551001 552001  
 553001 554001  
 555001 556001  
 557001 558001  
 559001 560001  
 561001 562001  
 563001 564001  
 565001 566001  
 567001 568001  
 569001 570001  
 571001 572001  
 573001 574001  
 575001 576001  
 577001 578001  
 579001 580001  
 581001 582001  
 583001 584001  
 585001 586001  
 587001 588001  
 589001 590001  
 591001 592001  
 593001 594001  
 595001 596001  
 597001 598001  
 599001 600001  
 601001 602001  
 603001 604001  
 605001 606001  
 607001 608001  
 609001 610001  
 611001 612001  
 613001 614001  
 615001 616001  
 617001 618001  
 619001 620001  
 621001 622001  
 623001 624001  
 625001 626001  
 627001 628001  
 629001 630001  
 631001 632001  
 633001 634001  
 635001 636001  
 637001 638001  
 639001 640001  
 641001 642001  
 643001 644001  
 645001 646001  
 647001 648001  
 649001 650001  
 651001 652001  
 653001 654001  
 655001 656001  
 657001 658001  
 659001 660001  
 661001 662001  
 663001 664001  
 665001 666001  
 667001 668001  
 669001 670001  
 671001 672001  
 673001 674001  
 675001 676001  
 677001 678001  
 679001 680001  
 681001 682001  
 683001 684001  
 685001 686001  
 687001 688001  
 689001 690001  
 691001 692001  
 693001 694001  
 695001 696001  
 697001 698001  
 699001 700001  
 701001 702001  
 703001 704001  
 705001 706001  
 707001 708001  
 709001 710001  
 711001 712001  
 713001 714001  
 715001 716001  
 717001 718001  
 719001 720001  
 721001 722001  
 723001 724001  
 725001 726001  
 727001 728001  
 729001 730001  
 731001 732001  
 733001 734001  
 735001 736001  
 737001 738001  
 739001 740001  
 741001 742001  
 743001 744001  
 745001 746001  
 747001 748001  
 749001 750001  
 751001 752001  
 753001 754001  
 755001 756001  
 757001 758001  
 759001 760001  
 761001 762001  
 763001 764001  
 765001 766001  
 767001 768001  
 769001 770001  
 771001 772001  
 773001 774001  
 775001 776001  
 777001 778001  
 779001 780001  
 781001 782001  
 783001 784001  
 785001 786001  
 787001 788001  
 789001 790001  
 791001 792001  
 793001 794001  
 795001 796001  
 797001 798001  
 799001 800001  
 801001 802001  
 803001 804001  
 805001 806001  
 807001 808001  
 809001 810001  
 811001 812001  
 813001 814001  
 815001 816001  
 817001 818001  
 819001 820001  
 821001 822001  
 823001 824001  
 825001 826001  
 827001 828001  
 829001 830001  
 831001 832001  
 833001 834001  
 835001 836001  
 837001 838001  
 839001 840001  
 841001 842001  
 843001 844001  
 845001 846001  
 847001 848001  
 849001 850001  
 851001 852001  
 853001 854001  
 855001 856001  
 857001 858001  
 859001 860001  
 861001 862001  
 863001 864001  
 865001 866001  
 867001 868001  
 869001 870001  
 871001 872001  
 873001 874001  
 875001 876001  
 877001 878001  
 879001 880001  
 881001 882001  
 883001 884001  
 885001 886001  
 887001 888001  
 889001 890001  
 891001 892001  
 893001 894001  
 895001 896001  
 897001 898001  
 899001 900001  
 901001 902001  
 903001 904001  
 905001 906001  
 907001 908001  
 909001 910001  
 911001 912001  
 913001 914001  
 915001 916001  
 917001 918001  
 919001 920001  
 921001 922001  
 923001 924001  
 925001 926001  
 927001 928001  
 929001 930001  
 931001 932001  
 933001 934001  
 935001 936001  
 937001 938001  
 939001 940001  
 941001 942001  
 943001 944001  
 945001 946001  
 947001 948001  
 949001 950001  
 951001 952001  
 953001 954001  
 955001 956001  
 957001 958001  
 959001 960001  
 961001 962001  
 963001 964001  
 965001 966001  
 967001 968001  
 969001 970001  
 971001 972001  
 973001 974001  
 975001 976001  
 977001 978001  
 979001 980001  
 981001 982001  
 983001 984001  
 985001 986001  
 987001 988001  
 989001 990001  
 991001 992001  
 993001 994001  
 995001 996001  
 997001 998001  
 999001 1000001



<212> DNA  
<213> Homo sapiens

<400> 72

```

accgagccga gcggaccgaa ggcgcgcccc agatgcaggt gagcaagagg atgctggcgg 60
ggggcgtag gagcatgccc agccccctcc tggcctgctg gcagcccatc ctctgctgg 120
tgctgggctc agtgctgtca ggctcgcca cgggctgccc gcccgcgtgc gaggctccg 180
cccaggaccg cgctgtgctg tgccaccgca agtgctttgt ggcagtcccc gagggcatcc 240
ccaccgagac gcgcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300
agttcgccag cttcccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
tgagagcccg cgcttcaac aacctcttca acctccggac gctgggtctc cgcagcaacc 420
gcctgaagct catcccgta ggctcttca ctggcctcag caacctgacc aagcaggaca 480
tcagcgagaa caagatcggt atcctactgg actacatgtt tcaggacctg tacaacctca 540
agtcactgga ggttggcgac aatgacctcg tctacatctc tcaccgcgcc ttcagcgggc 600
tcaacagcct ggagcagctg acgctggaga aatgcaacct gacctccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcatcgctc tgaggctccg gcacctcaac atcaatgcca 720
tccgggacta ctccctcaag aggctgtacc gactcaaggt cttggagatc tcccactggc 780
cctacttgga caccatgaca cccaactgcc tctacggcct caacctgacg tccctgtcca 840
tcacacactg caatctgacc gctgtgccct acctggccgt ccgccacctc gtctatctcc 900
gcttctcaa cctctcctac aaccccatca gcaccattga gggctccatg ttgcatgagc 960
tgctccggct gcaggagatc cagctggtgg gcgggcagct ggccgtggtg gagccctatg 1020
ccttcgcggc cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080
tgaggagaac agtcttccac tcggtgggca acctggagac actcatcctg gactccaacc 1140
cgctggcctg cgactgtcgg ctcctgtggg tgttccggcg ccgctggcgg ctcaacttca 1200
accggcagca gccacgtgc gccacgccc agtttgtcca gggcaaggag ttcaaggact 1260
tccctgatgt gctactgccc aactacttca cctgccgccg cgcccgcatc cgggaccgca 1320
aggcccagca ggtgtttgtg gacgagggcc acacggtgca gtttgtgtgc cgggccgatg 1380
gcgacccgcc gcccgccatc ctctggtctc caccgcgaaa gcacctggtc tcagccaaga 1440
gcaatgggcg gctcacagtc ttccctgatg gcacgctgga ggtgcgctac gcccaggtag 1500
aggacaacgg cacgtacctg tgcacgcgg ccaacgcggg cggcaacgac tccatgcccg 1560
cccacctgca tgtgcgcagc tactcgccc actggcccca tcagcccaac aagaccttcg 1620
ctttcatctc caaccagccg ggcgagggag aggccaacag caccgcgcc actgtgcctt 1680
tccccttga catcaagacc ctcatcatcg ccaccaccat gggcttcatc tctttcctgg 1740
gcgtcgctct cttctgctg gtgctgctgt ttctctggag ccggggcaag ggcaacacaa 1800
agcacaacat cgagatcgag tatgtgcccc gaaagtcgga cgcaggcatc agctccgccg 1860
acgcgccccg caagttcaac atgaagatga tatgagccg gggcggggg cagggacccc 1920
cgggcggccg ggcaggggaa ggggcctggt cgccacctgc tcaacttcca gtcttccca 1980
cctcctccct acccttctac acacgttctc tttctccctc ccgctccgt cccctgctgc 2040
cccccgccag ccctcaccac ctgccctcct tctaccagga cctcagaagc ccagacctgg 2100
ggacccacc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
aaaaaaaaa 2290

```

<210> 73  
<211> 620  
<212> PRT  
<213> Homo sapiens

<400> 73

```

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
  1                      5                      10                      15

```

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
                   20                  25                  30  
 Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
                   35                  40                  45  
 Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
           50                  55                  60  
 Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
       65                  70                  75                  80  
 Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
                   85                  90                  95  
 Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
                   100                  105                  110  
 Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
           115                  120                  125  
 Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
       130                  135                  140  
 Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
       145                  150                  155                  160  
 Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
                   165                  170                  175  
 Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
           180                  185                  190  
 Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
       195                  200                  205  
 Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
       210                  215                  220  
 Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
       225                  230                  235                  240  
 Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
           245                  250                  255  
 Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
           260                  265                  270  
 Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
       275                  280                  285  
 Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
       290                  295                  300

09303645-071001  
 T00T20S1050

Ser	Met	Leu	His	Glu	Leu	Leu	Arg	Leu	Gln	Glu	Ile	Gln	Leu	Val	Gly
305					310					315					320
Gly	Gln	Leu	Ala	Val	Val	Glu	Pro	Tyr	Ala	Phe	Arg	Gly	Leu	Asn	Tyr
				325					330					335	
Leu	Arg	Val	Leu	Asn	Val	Ser	Gly	Asn	Gln	Leu	Thr	Thr	Leu	Glu	Glu
			340					345					350		
Ser	Val	Phe	His	Ser	Val	Gly	Asn	Leu	Glu	Thr	Leu	Ile	Leu	Asp	Ser
		355					360					365			
Asn	Pro	Leu	Ala	Cys	Asp	Cys	Arg	Leu	Leu	Trp	Val	Phe	Arg	Arg	Arg
	370					375					380				
Trp	Arg	Leu	Asn	Phe	Asn	Arg	Gln	Gln	Pro	Thr	Cys	Ala	Thr	Pro	Glu
385					390					395					400
Phe	Val	Gln	Gly	Lys	Glu	Phe	Lys	Asp	Phe	Pro	Asp	Val	Leu	Leu	Pro
				405					410					415	
Asn	Tyr	Phe	Thr	Cys	Arg	Arg	Ala	Arg	Ile	Arg	Asp	Arg	Lys	Ala	Gln
			420					425					430		
Gln	Val	Phe	Val	Asp	Glu	Gly	His	Thr	Val	Gln	Phe	Val	Cys	Arg	Ala
		435					440					445			
Asp	Gly	Asp	Pro	Pro	Pro	Ala	Ile	Leu	Trp	Leu	Ser	Pro	Arg	Lys	His
	450					455					460				
Leu	Val	Ser	Ala	Lys	Ser	Asn	Gly	Arg	Leu	Thr	Val	Phe	Pro	Asp	Gly
465					470					475					480
Thr	Leu	Glu	Val	Arg	Tyr	Ala	Gln	Val	Gln	Asp	Asn	Gly	Thr	Tyr	Leu
				485					490					495	
Cys	Ile	Ala	Ala	Asn	Ala	Gly	Gly	Asn	Asp	Ser	Met	Pro	Ala	His	Leu
			500					505					510		
His	Val	Arg	Ser	Tyr	Ser	Pro	Asp	Trp	Pro	His	Gln	Pro	Asn	Lys	Thr
		515					520					525			
Phe	Ala	Phe	Ile	Ser	Asn	Gln	Pro	Gly	Glu	Gly	Glu	Ala	Asn	Ser	Thr
	530					535					540				
Arg	Ala	Thr	Val	Pro	Phe	Pro	Phe	Asp	Ile	Lys	Thr	Leu	Ile	Ile	Ala
545					550					555					560
Thr	Thr	Met	Gly	Phe	Ile	Ser	Phe	Leu	Gly	Val	Val	Leu	Phe	Cys	Leu
				565					570					575	
Val	Leu	Leu	Phe	Leu	Trp	Ser	Arg	Gly	Lys	Gly	Asn	Thr	Lys	His	Asn

580 585 590

Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser  
595 600 605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile  
610 615 620

<210> 74  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 74  
tcacctggag cctttattgg cc 22

<210> 75  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 75  
ataccagcta taaccaggct gcg 23

<210> 76  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 76  
caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg 50  
gg 52

<210> 77  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

24

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttgccga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 cccacgcgtc cgcacctcgg ccccgggctc cgaagcggct cggggggcgcc ctttcgggtca 60  
 acatcgtagt ccaccccctc cccatcccca gcccccgagg attcaggctc gccagcgccc 120  
 agccaggagg ccggccggga agcgcgatgg gggccccagc cgcctcgctc ctgctcctgc 180  
 tcctgctgtt cgcctgctgc tgggcgcccg gcggggccaa cctctcccag gacgacagcc 240  
 agccctggac atctgatgaa acagtgggtg ctggtggcac cgtggtgctc aagtgccaaag 300  
 tgaaagatca cgaggactca tccctgcaat ggtctaacc tgcctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct gggtacctct acgccccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtac acctgctcaa 480  
 tcttcactat gcctgtgcga actgccaaag cctcgtcac tgtgctagga attccacaga 540  
 agcccatcat cactggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600  
 gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaaaaggg gaccaagaac 660  
 tccacggaga accaaccgcg atacaggaag atcccaatgg taaaaccttc actgtcagca 720  
 gctcggtgac attccaggtt acccgggagg atgatggggc gagcatcgct tgcctctgtga 780  
 accatgaatc tctaaaggga gctgacagat ccacctctca acgcattgaa gttttatata 840  
 caccaactgc gatgattagg ccagaccctc cccatcctcg tgagggccag aagctgttgc 900  
 tacactgtga gggtcgcggc aatccagtc cccagcagta cctatgggag aaggaggcca 960  
 gtgtgccacc cctgaagatg acccaggaga gtgcctgat cttccctttc ctcaacaaga 1020  
 gtgacagtgg cacctacggc tgcacagcca ccagcaacat gggcagctac aaggcctact 1080  
 acaccctcaa tgttaatgac cccagtcagg tgccctctc ctccagcacc taccacgcca 1140  
 tcatcggttg gatcggtgct ttcattgtct tctgctgct catcatgctc atcttccttg 1200  
 gccactactt gatccggcac aaaggaacct acctgacaca tgaggcaaaa ggctccgacg 1260  
 atgctccaga cgcggacacg gccatcatca atgcagaagg cgggcagtca ggaggggacg 1320  
 acaagaagga atatttcac tagaggcgcc tgcccacttc ctgcgcccc cagggggcct 1380  
 gtggggactg ctggggccgt caccaaccgc gacttgtaca gagcaaccgc agggccgccc 1440  
 ctcccgtctg ctcccagcc caccacccc cctgtacaga atgtctgctt tgggtgcggg 1500  
 tttgtactcg gtttggaatg gggagggagg agggcggggg gaggggaggg ttgccctcag 1560  
 ccctttccgt ggcttctctg catttggtt attattatt ttgtaacaa cccaaatcaa 1620  
 atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa aacaaacaaa 1680  
 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala  
 1 5 10 15  
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
 20 25 30  
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45  
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60  
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80  
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95  
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110  
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125  
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140  
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160  
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175  
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190  
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205  
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220  
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240  
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255  
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270  
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic



## oligonucleotide probe

<400> 87  
cctagcacag tgacgaggga cttggc 26

<210> 88

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 88  
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 89  
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90

<211> 2755

<212> DNA

<213> Homo sapiens

<400> 90  
ggggggttagg gaggaaggaa tccacccccca ccccccaaa cccttttctt ctccttttct 60  
ggcttcggac attggagcac taaatgaact tgaattgtgt ctgtggcgag caggatggtc 120  
gctgttactt tgtgatgaga tcggggatga attgctcgct ttaaaaatgc tgctttggat 180  
tctgttgctg gagacgtctc tttgttttgc cgctggaaac gttacagggg acgtttgcaa 240  
agagaagatc tgttcctgca atgagataga aggggacctc cacgtagact gtgaaaaaaa 300  
gggcttcaca agtctgcagc gtttcaactgc cccgacttcc cagttttacc atttatttct 360  
gcatggcaat tccctcactc gacttttccc taatgagttc gctaactttt ataatgcggt 420  
tagtttgcac atggaaaaca atggcttgca tgaaatcggt ccggggggtt ttctggggct 480  
gcagctgggtg aaaaggctgc acatcaacaa caacaagatc aagtcttttc gaaagcagac 540  
ttttctgggg ctggacgata tggaaatatc ccaggctgat ttaatttat tacgagatat 600  
agaccggggg gccttccagg acttgaacaa gctggagggtg ctcattttta atgacaatct 660  
catcagcacc ctacctgcca acgtgttcca gtatgtgccc atcaccacc tcgacctccg 720  
gggtaacagg ctgaaaacgc tgccctatga ggaggtcttg gagcaaatcc ctgggtattgc 780  
ggagatcctg ctagaggata acccttggga ctgcacctgt gatctgctct ccctgaaaga 840  
atggctggaa aacattccca agaatgccct gatcggccga gtggctctgcg aagccccac 900  
cagactgcag ggtaaagacc tcaatgaaac caccgaacag gacttgtgtc ctttgaaaaa 960  
ccgagtggat tctagtctcc cggcgcccc tgcccaagaa gagaccttg ctcctggacc 1020  
cctgccaaact cctttcaaga caaatgggca agaggatcat gccacaccag ggtctgctcc 1080

aaacggaggt acaaagatcc caggcaactg gcagatcaaa atcagaccca cagcagcgat 1140  
 agcgacgggt agctccagga acaaaccctt agctaacagt ttaccctgcc ctgggggctg 1200  
 cagctgcgac cacatcccag ggtcgggttt aaagatgaac tgcaacaaca ggaacgtgag 1260  
 cagcttggct gatttgaagc ccaagctctc taacgtgcag gagcttttcc tacgagataa 1320  
 caagatccac agcatccgaa aatcgcaact tgtggattac aagaacctca ttctgttgga 1380  
 tctgggcaac aataacatcg ctactgtaga gaacaacact ttcaagaacc ttttggacct 1440  
 caggtggcta tacatggata gcaattacct ggacacgctg tcccgggaga aattcgcggtg 1500  
 gctgcaaaac ctagagtacc tgaacgtgga gtacaacgct atccagctca tcctcccggtg 1560  
 cactttcaat gccatgcccc aactgaggat cctcattctc aacaacaacc tgctgaggtc 1620  
 cctgcctgtg gacgtgttcg ctgggtctc gctctctaaa ctgagcctgc acaacaatta 1680  
 cttcatgtac ctcccgtgtg caggggtgct ggaccagtta acctccatca tccagataga 1740  
 cctccacgga aaccctgtgg agtgctcctg cacaattgtg cctttcaagc agtgggcaga 1800  
 acgcttgggt tccgaagtgc tgatgagcga cctcaagtgt gagacgccgg tgaacttctt 1860  
 tagaaaggat ttcatgctcc tctccaatga cgagatctgc cctcagctgt acgctaggat 1920  
 ctgccccacg ttaacttcgc acagtaaaaa cagcactggg ttggcggaga cggggacgca 1980  
 ctccaactcc tacctagaca ccagcagggt gtccatctcg gtgttggtcc cgggactgct 2040  
 gctggtgttt gtcacctccg ccttcaccgt ggtgggcatg ctctgtttta tcctgaggaa 2100  
 ccgaaagcgg tccaagagac gagatgccaa ctctcccgcg tccgagatta attccctaca 2160  
 gacagtctgt gactcttcct actggcaca tgggccttac aacgcagatg gggcccacag 2220  
 agtgtatgac tgtggctctc actcgctctc agactaagac cccaacccca ataggggagg 2280  
 gcagagggaa ggcgatacat ccttccccac cgcaggcacc cgggggctg gagggcggtg 2340  
 taccctaaatc ccgcgcat cagcctggat gggcataagt agataaataa ctgtgagctc 2400  
 gcacaaccga aagggcctga ccccttactt agctccctcc ttgaaacaaa gagcagactg 2460  
 tggagagctg ggagagcgca gccagctcgc tctttgctga gagcccttt tgacagaaag 2520  
 cccagcacga ccctgctgga agaactgaca gtgccctcgc cctcgcccc ggggcctgtg 2580  
 ggggttgatg ccgcggttct atacatatat acatatatcc acatctatat agagagatag 2640  
 atatctattt ttccctgtg gattagcccc gtgatggctc cctgttggt acgcagggat 2700  
 gggcagttgc acgaaggcat gaatgtattg taaataagta actttgactt ctgac 2755

<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala  
 1 5 10 15

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn  
 20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr  
 35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe  
 50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn  
 65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu  
 85 90 95

Ile	Val	Pro	Gly 100	Ala	Phe	Leu	Gly	Leu	Gln	Leu	Val	Lys	Arg	Leu	His
Ile	Asn	Asn	Asn 115	Lys	Ile	Lys	Ser	Phe	Arg	Lys	Gln	Thr	Phe	Leu	Gly
Leu	Asp	Asp	Leu 130	Glu	Tyr	Leu	Gln	Ala	Asp	Phe	Asn	Leu	Leu	Arg	Asp
Ile	Asp	Pro	Gly 145	Ala	Phe 150	Gln	Asp	Leu	Asn	Lys 155	Leu	Glu	Val	Leu	Ile 160
Leu	Asn	Asp	Asn 165	Leu	Ile	Ser	Thr	Leu	Pro	Ala	Asn	Val	Phe	Gln	Tyr 175
Val	Pro	Ile	Thr 180	His	Leu	Asp	Leu	Arg	Gly	Asn	Arg	Leu	Lys	Thr	Leu
Pro	Tyr	Glu	Glu 195	Val	Leu	Glu	Gln	Ile	Pro	Gly	Ile	Ala	Glu	Ile	Leu
Leu	Glu	Asp	Asn 210	Pro	Trp	Asp	Cys	Thr	Cys	Asp	Leu	Leu	Ser	Leu	Lys
Glu	Trp	Leu	Glu 225	Asn	Ile 230	Pro	Lys	Asn	Ala	Leu	Ile	Gly	Arg	Val	Val 240
Cys	Glu	Ala	Pro 245	Thr	Arg	Leu	Gln	Gly	Lys	Asp	Leu	Asn	Glu	Thr	Thr 255
Glu	Gln	Asp	Leu 260	Cys	Pro	Leu	Lys	Asn	Arg	Val	Asp	Ser	Ser	Leu	Pro
Ala	Pro	Pro	Ala 275	Gln	Glu	Glu	Thr	Phe	Ala	Pro	Gly	Pro	Leu	Pro	Thr
Pro	Phe	Lys	Thr 290	Asn	Gly	Gln	Glu	Asp	His	Ala	Thr	Pro	Gly	Ser	Ala
Pro	Asn	Gly	Gly 305	Thr	Lys	Ile	Pro	Gly	Asn	Trp	Gln	Ile	Lys	Ile	Arg 320
Pro	Thr	Ala	Ala 325	Ile	Ala	Thr	Gly	Ser	Ser	Arg	Asn	Lys	Pro	Leu	Ala
Asn	Ser	Leu	Pro 340	Cys	Pro	Gly	Gly	Cys	Ser	Cys	Asp	His	Ile	Pro	Gly
Ser	Gly	Leu	Lys 355	Met	Asn	Cys	Asn	Asn	Arg	Asn	Val	Ser	Ser	Leu	Ala
Asp	Leu	Lys	Pro 370	Lys	Leu	Ser	Asn	Val	Gln	Glu	Leu	Phe	Leu	Arg	Asp

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

45

gaggggaagg gaggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240  
 ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300  
 ggggcctcag agaatgaggc cggcggttcgc cctgtgcctc ctctggcagg cgtctgggc 360  
 cgggcccggg ggcggcgaac accccactgc cgaccgtgct ggctgctcgg cctcgggggc 420  
 ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcatect 480  
 gcgaggtggg gcgctcagca cegtgcgtgc gggcgccgag ctgcgcgctg tgctgcgct 540  
 cctgcgggca ggcccagggc cgggaggggg ctccaaagac ctgctgttct gggtcgcact 600  
 ggagcgcagg cgttcccact gcaccctgga gaacgagcct ttgcggggtt tctcctggct 660  
 gtcctccgac cccggcggtc tcgaaagcga cacgctgcag tgggtggagg agccccaacg 720  
 ctctgcacc gcgcgggat gcgcggtact ccaggccacc ggtggggctg agcccgagg 780  
 ctggaaggag atgcgatgcc acctgcgcgc caacggctac ctgtgcaagt accagtttga 840  
 ggtcttgtgt cctgcgccgc gccccggggc cgctcctaac ttgagctatc gcgcgccctt 900  
 ccagctgcac agcgccgctc tggacttcag tccacctggg accgaggtga gtgcgctctg 960  
 cgggggacag ctcccgatct cagttacttg catcgcgagc gaaatcggcg ctgcgtggga 1020  
 caaactctcg ggcgatgtgt tgtgtccctg ccccgggagg tacctccgtg ctggcaaagt 1080  
 cgcagagctc cctaactgcc tagacgactt gggaggcttt gcctgcgaat gtgctacggg 1140  
 cttcgagctg gggaaggacg gccgctcttg tgtgaccagt ggggaaggac agccgaccct 1200  
 tggggggacc ggggtgcccc ccaggcgccc gccggccact gcaaccagcc cegtgcgcga 1260  
 gagaacattg ccaatcaggg tcgacgagaa gctgggagag acaccacttg tccctgaaca 1320  
 agacaattca gtaacatcta ttcctgagat tcctcgatgg ggatcacaga gcacgatgtc 1380  
 tacccttcaa atgtcccttc aagccgagtc aaaggccact atcaccccat cagggagcgt 1440  
 gatttccaag tttaattcta cgacttcctc tgccactcct caggctttcg actcctcctc 1500  
 tgccgtggtc ttcataattg tgagcacagc agtagtagtg ttggtgatct tgaccatgac 1560  
 agtactgggg cttgtcaagc tctgctttca cgaaagcccc tcttcccagc caagggaagg 1620  
 gtctatgggc ccgccgggccc tggagagtga tcctgagccc gctgctttgg gctccagttc 1680  
 tgcacattgc acaacaatg ggggtgaaagt cggggactgt gatctgcggg acagagcaga 1740  
 ggggtgcctt ctggcggagt cccctcttgg ctctagtgt gcatagggaa acaggggaca 1800  
 tgggcactcc tgtgaacagt ttttcacttt tgatgaaacg gggaaccaag aggaacttac 1860  
 ttgtgtaact gacaatttct gcagaaatcc cccttcctct aaattccctt tactccactg 1920  
 aggagctaaa tcagaactgc acactccttc cctgatgata gaggaagtgg aagtgccttt 1980  
 aggatggtga tactggggga ccgggtagtg ctggggagag atatcttctt atgtttattc 2040  
 ggagaatttg gagaagtgt tgaacttttc aagacattgg aaacaaatag aacacaatat 2100  
 aatttacatt aaaaaataat ttctacaaa atggaaagga aatgttctat gttgttcagg 2160  
 ctaggagtat attggttcga aatcccaggg aaaaaataa aaataaaaaa ttaaaggatt 2220  
 gttgat 2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro  
 1 5 10 15

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

Arg 65	Ala	Gly	Ala	Glu	Leu	Arg	Ala	Val	Leu	Ala	Leu	Leu	Arg	Ala	Gly 80
Pro	Gly	Pro	Gly	Gly 85	Gly	Ser	Lys	Asp	Leu 90	Leu	Phe	Trp	Val	Ala	Leu 95
Glu	Arg	Arg	Arg 100	Ser	His	Cys	Thr	Leu 105	Glu	Asn	Glu	Pro	Leu 110	Arg	Gly
Phe	Ser	Trp 115	Leu	Ser	Ser	Asp	Pro 120	Gly	Gly	Leu	Glu	Ser 125	Asp	Thr	Leu
Gln 130	Trp	Val	Glu	Glu	Pro	Gln 135	Arg	Ser	Cys	Thr	Ala 140	Arg	Arg	Cys	Ala
Val 145	Leu	Gln	Ala	Thr	Gly 150	Gly	Val	Glu	Pro 155	Ala	Gly	Trp	Lys	Glu	Met 160
Arg	Cys	His	Leu 165	Arg	Ala	Asn	Gly	Tyr 170	Leu	Cys	Lys	Tyr	Gln	Phe 175	Glu
Val	Leu	Cys 180	Pro	Ala	Pro	Arg	Pro	Gly 185	Ala	Ala	Ser	Asn	Leu 190	Ser	Tyr
Arg	Ala	Pro 195	Phe	Gln	Leu	His	Ser 200	Ala	Ala	Leu	Asp	Phe 205	Ser	Pro	Pro
Gly 210	Thr	Glu	Val	Ser	Ala	Leu 215	Cys	Arg	Gly	Gln	Leu 220	Pro	Ile	Ser	Val
Thr 225	Cys	Ile	Ala	Asp	Glu 230	Ile	Gly	Ala	Arg	Trp 235	Asp	Lys	Leu	Ser	Gly 240
Asp	Val	Leu	Cys 245	Pro	Cys	Pro	Gly	Arg	Tyr 250	Leu	Arg	Ala	Gly	Lys 255	Cys
Ala	Glu	Leu	Pro 260	Asn	Cys	Leu	Asp	Asp 265	Leu	Gly	Gly	Phe	Ala 270	Cys	Glu
Cys	Ala	Thr 275	Gly	Phe	Glu	Leu	Gly	Lys	Asp 280	Gly	Arg	Ser 285	Cys	Val	Thr
Ser 290	Gly	Glu	Gly	Gln	Pro	Thr 295	Leu	Gly	Gly	Thr	Gly 300	Val	Pro	Thr	Arg
Arg 305	Pro	Pro	Ala	Thr	Ala 310	Thr	Ser	Pro	Val	Pro 315	Gln	Arg	Thr	Trp	Pro 320
Ile	Arg	Val	Asp	Glu 325	Lys	Leu	Gly	Glu	Thr 330	Pro	Leu	Val	Pro	Glu 335	Gln
Asp	Asn	Ser	Val	Thr	Ser	Ile	Pro	Glu	Ile	Pro	Arg	Trp	Gly	Ser	Gln

	340		345		350
Ser Thr Met	Ser Thr Leu Gln Met	Ser Leu Gln Ala Glu	Ser Lys Ala		
355	360	365			
Thr Ile Thr	Pro Ser Gly Ser Val	Ile Ser Lys Phe Asn	Ser Thr Thr		
370	375	380			
Ser Ser Ala	Thr Pro Gln Ala Phe Asp	Ser Ser Ser Ala Val	Val Phe		
385	390	395	400		
Ile Phe Val	Ser Thr Ala Val Val Val	Leu Val Ile Leu Thr	Met Thr		
	405	410	415		
Val Leu Gly	Leu Val Lys Leu Cys Phe His	Glu Ser Pro Ser Ser	Gln		
	420	425	430		
Pro Arg Lys	Glu Ser Met Gly Pro Pro	Gly Leu Glu Ser Asp	Pro Glu		
	435	440	445		
Pro Ala Ala	Leu Gly Ser Ser Ser	Ala His Cys Thr Asn	Asn Gly Val		
	450	455	460		
Lys Val Gly	Asp Cys Asp Leu Arg Asp Arg	Ala Glu Gly Ala Leu	Leu		
465	470	475	480		
Ala Glu Ser	Pro Leu Gly Ser Ser	Asp Ala			
	485	490			

&lt;210&gt; 97

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 97

tggaaggaga tgcgatgccca cctg

24

&lt;210&gt; 98

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 98

tgaccagtgg ggaaggacag

20



<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 99  
 acagagcaga gggcgccttg 20  
  
 <210> 100  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 100  
 tcagggacaa gtggtgtctc tccc 24  
  
 <210> 101  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 101  
 tcagggaagg agtgtgcagt tctg 24  
  
 <210> 102  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 102  
 acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct 50  
  
 <210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 103

```

cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgccct gccggccgcg 120
tatcccccg ctacctgggc cgcgccgcgg cgggtgcgcgc gtgagagggg gcgcgcgggc 180
agccgagcgc cgggtgtgagc cagcgcgtgct gccagtgtga gcggcggtgt gagcgcgggtg 240
gggtgcggagg ggcgtgtgtg ccggcgcgcg cgcctgtggg tgcaaaccac gagcgtctac 300
gctgccatga ggggcgcgaa cgccctgggc ccactctgcc tgctgtctggc tgccgccacc 360
cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420
ggagagtctg gattttattgg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
tgtacttggg aaatcacagt tcccgaagga aaagtagtcg ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgccgctat gactttgtgg atgtgtacaa tggccatgcc 600
aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgtgtccagt 660
ggcaacaaga tgatggtgca gatgatttct gatgccaaca cagctggcaa tggcttcatg 720
gccatgttct ccgctgctga accaaacgaa agaggggatc agtattgtgg aggactcctt 780
gacagacctt ccggtctttt taaaaccccc aactggccag accgggatta ccctgcagga 840
gtcacttgtg tgtggcacat tgtagcccca aagaatcagc ttatagaatt aaagtttgag 900
aagtttgatg tggagcgaga taactactgc cgatatgatt atgtggctgt gtttaatggc 960
ggggaagtca acgatgctag aagaattgga aagtattgtg gtgatagtc accctgcgcca 1020
attgtgtctg agagaaatga acttcttatt cagtttttat cagacttaag ttttaactga 1080
gatgggttta ttggtcacta catattcagg ccaaaaaaac tgcctacaac tacagaacag 1140
cctgtcacca ccacattccc tgtaaccacg ggtttaaaac ccaccgtggc cttgtgtcaa 1200
caaaagtgtg gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtatta 1260
gccggcactg ttatcacaac catcactcgc gatgggagtt tgcacgccac agtctcgatc 1320
atcaacatct acaaagaggg aaatttggcg attcagcagg cgggcaagaa catgagtgcc 1380
aggctgactg tcgtctgcaa gcagtgcctt ctctcagaa gaggtctaaa ttacattatt 1440
atggggccaag taggtgaaga tgggcgaggc aaaatcatgc caaacagctt tatcatgatg 1500
ttcaagacca agaatcagaa gctcctggat gccttaaaaa ataagcaatg ttaacagtga 1560
actgtgtcca tttaagctgt attctgccat tgcctttgaa agatctatgt tctctcagta 1620
gaaaaaaaaa tacttataaa attacatatt ctgaaagagg attccgaaag atgggactgg 1680
ttgactcttc acatgatgga ggtatgaggc ctccgagata gctgagggaa gttctttgcc 1740
tgctgtcaga ggagcagcta tctgattgga aacctgccga cttagtgcgg tgataggaag 1800
ctaaaagtgt caagcgttga cagcttgga gcggtttatt atacatctct gtaaaaggat 1860
attttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920
gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tottgcggtt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1                      5                      10                      15

```

```

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
                20                      25                      30

```

```

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
        35                      40                      45

```

```

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
        50                      55                      60

```

Val 65	Pro	Glu	Gly	Lys	Val 70	Val	Val	Leu	Asn	Phe 75	Arg	Phe	Ile	Asp	Leu 80
Glu	Ser	Asp	Asn	Leu 85	Cys	Arg	Tyr	Asp	Phe 90	Val	Asp	Val	Tyr	Asn 95	Gly
His	Ala	Asn	Gly 100	Gln	Arg	Ile	Gly	Arg	Phe 105	Cys	Gly	Thr	Phe 110	Arg	Pro
Gly	Ala	Leu 115	Val	Ser	Ser	Gly	Asn	Lys	Met	Met	Val	Gln 125	Met	Ile	Ser
Asp	Ala 130	Asn	Thr	Ala	Gly	Asn 135	Gly	Phe	Met	Ala	Met 140	Phe	Ser	Ala	Ala
Glu 145	Pro	Asn	Glu	Arg	Gly 150	Asp	Gln	Tyr	Cys	Gly 155	Gly	Leu	Leu	Asp	Arg 160
Pro	Ser	Gly	Ser	Phe 165	Lys	Thr	Pro	Asn	Trp 170	Pro	Asp	Arg	Asp	Tyr 175	Pro
Ala	Gly	Val	Thr 180	Cys	Val	Trp	His	Ile 185	Val	Ala	Pro	Lys	Asn 190	Gln	Leu
Ile	Glu	Leu 195	Lys	Phe	Glu	Lys	Phe	Asp 200	Val	Glu	Arg	Asp 205	Asn	Tyr	Cys
Arg	Tyr 210	Asp	Tyr	Val	Ala	Val 215	Phe	Asn	Gly	Gly	Glu 220	Val	Asn	Asp	Ala
Arg 225	Arg	Ile	Gly	Lys	Tyr 230	Cys	Gly	Asp	Ser	Pro 235	Pro	Ala	Pro	Ile	Val 240
Ser	Glu	Arg	Asn 245	Glu	Leu	Leu	Ile	Gln	Phe 250	Leu	Ser	Asp	Leu 255	Ser	Leu
Thr	Ala	Asp	Gly 260	Phe	Ile	Gly	His	Tyr 265	Ile	Phe	Arg	Pro	Lys 270	Lys	Leu
Pro	Thr 275	Thr	Thr	Glu	Gln	Pro	Val	Thr 280	Thr	Thr	Phe	Pro 285	Val	Thr	Thr
Gly 290	Leu	Lys	Pro	Thr	Val	Ala 295	Leu	Cys	Gln	Gln	Lys 300	Cys	Arg	Arg	Thr
Gly 305	Thr	Leu	Glu	Gly	Asn 310	Tyr	Cys	Ser	Ser	Asp 315	Phe	Val	Leu	Ala	Gly 320
Thr	Val	Ile	Thr 325	Thr	Ile	Thr	Arg	Asp	Gly 330	Ser	Leu	His	Ala 335	Thr	Val
Ser	Ile	Ile	Asn	Ile	Tyr	Lys	Glu	Gly	Asn	Leu	Ala	Ile	Gln	Gln	Ala

340	345	350
Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro		
355	360	365
Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu		
370	375	380
Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys		
385	390	400
Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys		
405	410	415

&lt;210&gt; 105

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 105

ccgattcata gacctcgaga gt

22

&lt;210&gt; 106

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 106

gtcaaggagt cctccacaat ac

22

&lt;210&gt; 107

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

&lt;210&gt; 108

&lt;211&gt; 1838

&lt;212&gt; DNA

"T00T20" C3T3T5T0

<213> Homo sapiens

<400> 108

```

cggacgcgtg ggcggacgcg tgggcggccc acggcgcccc cgggctgggg cggtcgcttc 60
ttccttctcc gtggcctacg aggggtcccca gcctgggtaa agatggcccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctcagcctct tctcaacct cccaggacct 180
atctggctcc agccctctcc acctccccag tcttctcccc cgctcagcc ccatccgtgt 240
catacctgcc ggggactggt tgacagcttt aacaagggcc tggagagaac catccgggac 300
aactttggag gtggaaacac tgctggggag gaagagaatt tgtccaaata caaagacagt 360
gagacccgcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtggcac 420
cgcttctggt agctgagtga ggagctgggt gagagctggt ggtttcacaa gcagcaggag 480
gccccggacc tcttccagtg gctgtgctca gattccctga agctctgctg ccccgagggc 540
accttcgggc cctcctgcct tccctgtcct gggggaacag agaggccctg cgggtggctac 600
gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtgactg ccaagccggc 660
tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720
agccatctgg tatgttcggc ttgttttggc ccctgtgcc gatgctcagg acctgaggaa 780
tcaaactgtt tgcaatgcaa gaagggtggt gccctgcac acctcaagtg tgtagacatt 840
gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgcgt gaacactgag 900
ggctcctatg agtgccgaga ctgtgccaaag gctgcctag gctgcatggg ggcagggcca 960
ggtcgctgta agaagtgtag ccctggctat cagcaggtgg gctccaagtg tctcgatgtg 1020
gatgagtgtg agacagaggt gtgtccggga gagaacaagc agtgtgaaaa caccgagggc 1080
ggttatcgct gcactctgtc cgagggctac aagcagatgg aaggcatctg tgtgaaggag 1140
cagatcccag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtggtgctg 1200
cagcagatgt tctttggcat catcatctgt gcactggcca cgctggctgc taaggcgac 1260
ttggtgttca ccgccatctt cattggggct gtggcggcca tgactggcta ctggttgtca 1320
gagcgcagtg accgtgtgct ggagggcttc atcaaggcca gataatcgcg gccaccacct 1380
gtaggacctc ctcccaccca cgctgcccc agagcttggg ctgccctcct gctggacact 1440
caggacagct tggtttatatt ttgagagtgg ggtaagcacc cctacctgcc ttacagagca 1500
gcccaggtag ccaggcccg gacagacaagg cccctgggg aaaaagtagc cctgaagggtg 1560
gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620
agtttttct taatgggtgg tgetagagct ttggccctg cttaggatta ggtggtcctc 1680
acaggggtgg ggccatcaca gctccctcct gccagctgca tgctgccagt tcctgttctg 1740
tgttcaccac atccccacac ccatttgcca cttatttatt catctcagga aataaagaaa 1800
ggtcttgga agttaaaaaa aaaaaaaaaa aaaaaaaa 1838

```

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

```

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1              5              10              15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20              25              30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35              40              45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50              55              60

```

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80  
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95  
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110  
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125  
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140  
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160  
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175  
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190  
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205  
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220  
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240  
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255  
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270  
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285  
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300  
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320  
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335  
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

09902615.074004

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
           355                                  360                                  365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
      370                                  375                                  380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385                                  390                                  395                                  400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
                                   405                                  410                                  415

Ile Lys Gly Arg  
                   420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac

22

<210> 113

090916.0400  
 15:54:50

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
 tgagaccctc ctgcagcctt ctcaagggac agccccactc tgcctcttgc tcctccaggg 60  
 cagcaccatg cagcccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120  
 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcacccccca cccacgtgag 240  
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagagggt 300  
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360  
 gctggtgttc ggcatggagc agcggctgcc gcccacagc gagctggtgc aggcctgct 420  
 gcggctcttc caggagccgg tcccccaagg cgcgctgcac aggcacgggc ggctgtcccc 480  
 gcgcagcgcc cgggcccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540  
 ccgcacctcc ctcatcgact ccaggctggt gtccgtccac gagagcggct ggaaggcctt 600  
 cgacgtgacc gaggccgtga acttctggca gcagctgagc cggccccggc agccgctgct 660  
 gctacagggtg tcggtgcaga gggagcatct gggcccgtg gcgtccggcg cccacaagct 720  
 ggtccgcttt gctcgcagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780  
 caccctggac cttggggact atggagctca gggcgactgt gacctgaag caccaatgac 840  
 cgagggcacc cgctgctgcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900  
 cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960  
 gcagcccccg gaggccctgg ccttcaagtg gccgtttctg gggcctcgac agtgcacgc 1020  
 ctcgagact gactcgctgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080  
 ccaggtggtc agcctgcccc acatgagggt gcagaagtgc agctgtgcct cggatggtgc 1140  
 gctcgtgcca aggaggtcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200  
 gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgctgat 1260  
 ggacaaatgc tctgtgctct ctagttagcc ctgaatttgc ttcctctgac aagttacctc 1320  
 acctaatatt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380  
 ttctctattc ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440  
 acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500  
 aaagtcctcc accaccactc tggacctaag acctgggggt aagtgtgggt tgtgcatccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
 1 5 10 15  
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45



Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285  
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

gtctgttccc	aggagtcctt	cggcggctgt	tgtgtcagtg	gcctgatcgc	gatggggaca	60
aaggcgcaag	tcgagaggaa	actgttgtgc	ctcttcata	tggcgatcct	gttgtgctcc	120
ctggcattgg	gcagtgttac	agtgcactct	tctgaacctg	aagtcagaat	tcctgagaat	180

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240  
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300  
gaggaccggg tgaccttctt gccactgggt atcaccttca agtccgtgac acgggaagac 360  
actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420  
gtcaagctca tctgtcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480  
accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc accttctgaa 540  
tacacctggt tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac cctgaccttc 600  
agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tccccgtca 660  
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720  
tcaaagtctg tgcgcatgga agctgtggag cggaatgtgg gggatcatcg ggcagccgtc 780  
cttgtaacct tgattctcct gggaatcttg gtttttggca tctgggttgc ctatagccga 840  
ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900  
agtgcgccga gtgaaggaga attcaaacag acctcgatcat tcttgggtgtg agcctgggtc 960  
gctcaccgcc tatcatctgc atttgcttta cttaggtgct accggactct ggcctctgat 1020  
gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc cctacttct 1080  
tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140  
tttctacca ctgctgagt gcttggaaact tgtttaaagt gtttattccc catttctttg 1200  
agggatcagg aaggaatcct gggatgcca ttgacttccc ttctaagtag acagcaaaaa 1260  
tggcgggggt cgcaggaatc tgcactcaac tgcccacttg gctggcaggg atctttgaat 1320  
aggtatcttg agcttgggtc tgggctcttt ccttgtgtac tgacgaccag ggcagctgt 1380  
tctagagcgg gaattagagg cttagagcggc tgaaatgggt gtttgggtgat gacactgggg 1440  
tccttccatc tctggggccc actctcttct gtcttcccat gggaaagtgc actgggatcc 1500  
ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560  
agctcttgtt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggattttaa 1620  
accgctgtc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680  
cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740  
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tggatcatgc ctgtagtccc 1800  
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
                   100                  105                  110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
                   115                  120                  125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
                   130                  135                  140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
                   145                  150                  155                  160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
                   165                  170                  175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
                   180                  185                  190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
                   195                  200                  205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
                   210                  215                  220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
                   225                  230                  235                  240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
                   245                  250                  255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
                   260                  265                  270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
                   275                  280                  285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
                   290                  295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 120

tgcgcggagct gtgttctggt tccc

24

<210> 121

<211> 50

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 121  
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50  
  
 <210> 122  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 122  
 acacctgggtt caaagatggg 20  
  
 <210> 123  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 123  
 taggaagagt tgctgaaggc acgg 24  
  
 <210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 124  
 ttgccttact caggtgctac 20  
  
 <210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 125

20

 $\langle 211 \rangle$  1210

<212> DNA

<213> Homo sapiens

cagcgcgtgg	cggcgccgc	tgtggggaca	gcatagagcgg	cgggttggatg	gcgcaggttg	60
gagctgtggcg	aacaggggcct	ctgggccttg	cgctgctgct	gctgctcggc	ctcggactag	120
gcctggaggc	cgccgcgagc	ccgctttcca	ccccgacctc	tgcccaggcc	gcaggcccca	180
gctcaggctc	gtgccacccc	accaagtctc	agtgcgcac	cagtggctta	tgcgtgcccc	240
tcacctggcg	ctgcgacagg	gacttggact	gcagcgatgg	cagcgatgag	gaggagtgca	300
ggattgagcc	atgtacccag	aaagggcaat	gccaccgcgc	ccctggcctc	ccctgcccct	360
gcaccggcgt	cagtgactgc	tctgggggaa	ctgacaagaa	actgcgcaac	tgcagccgcc	420
tggcctgcct	agcaggcgag	ctccgttgca	cgctgagcga	tgactgcatt	ccactcacgt	480
ggcgctgcga	cggccaccca	gactgtcccc	actccagcga	cgagctcggc	tgtggaacca	540
atgagatcct	cccgaagagg	gatgccacaa	ccatggggcc	ccctgtgacc	ctggagagtg	600
tcacctctct	caggaatgcc	acaacccatg	ggccccctgt	gaccctggag	agtgtcccct	660
ctgtcgggaa	tgcacatcc	tcctctgcgc	gagaccagtc	tggaaagcca	actgcctatg	720
gggttattgc	agctgctgcg	gtgctcagtg	caagcctggg	caccgccacc	ctcctccttt	780
tgtcctggct	ccgagcccag	gagcgcctcc	gccactggg	gttactggtg	gccatgaagg	840
agtcacctgct	gctgtcagaa	cagaagacct	cgctgccttg	aggacaagca	cttgccacca	900
ccgtcactca	gccctgggcg	tagccggaca	ggaggagagc	agtgatgcgg	atgggtacct	960
gggcacacca	gccctcagag	acctgagttc	ttctggccac	gtggaacctc	gaacccgagc	1020
tcctgcagaa	gtggcccttg	agattgaggg	tccttgagca	ctccctatgg	agatccgggg	1080
agctaggatg	gggaacctgc	cacagccaga	actgaggggc	tggccccagg	cagctcccag	1140
ggggtagaac	ggccctgtgc	ttaagacact	ccctgctgcc	ccgtctgagg	gtggcgatta	1200
aaqttgcttc						1210

<210> 127

<211> 282

&lt;212&gt; PRT

<213> Homo sapiens

<400> 127

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                             85                            90                            95  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                             100                            105                            110  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                             115                            120                            125  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                             130                            135                            140  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                             145                            150                            155                            160  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                             165                            170                            175  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                             180                            185                            190  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                             195                            200                            205  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                             210                            215                            220  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala  
                             225                            230                            235                            240  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                             245                            250                            255  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                             260                            265                            270  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                             275                            280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129

ttggttccac agccgagctc gtcg

24

<210> 130

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130

gaggaggagt gcaggattga gccatgtacc cagaaaagggc aatgcccacc

50

<210> 131

<211> 1843

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1837)

<223> a, t, c or g

<400> 131

```

cccacgcgtc cggctctcgt cgctcgcgca gcggcggcag cagaggtcgc gcacagatgc 60
gggttagact ggcgggggga ggaggcggag gagggaagga agctgcatgc atgagacca 120
cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccoga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcctg tggtttcagc tggcgtctgt cttcggccct gcacagctca 300
cgggcggtt cgatgacctt caagtgtgtg ctgaccccg cattcccag aatggcttca 360
ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatac 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600
atgaaggatt caagatccgg taccgccgac tacacaatat ggtttcatta tgtcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
atcgtctgct tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
ctccaatggt ggtcagcaga gatttcgtct gccacccgag gccttgtagc cgctacaacc 960
acggaactgt ggtggagttt tactgcgata ctggctacag cctcaccagc gactacaagt 1020
acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatcag 1080
agcaaactg gccagcacc catgagaccc tcctgaccac gtggaagatt gtggcggttca 1140

```



cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200  
 agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260  
 ttgtgggtgt agacggcgtg cccgtcatgc tcccgctcta tgacgaagct gtgagtggcg 1320  
 gcttgagtgc cttaggcccc gggtacatgg cctctgtggg ccagggtctgc cccttaccgg 1380  
 tggacgacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440  
 agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500  
 ctcccaggtg ccaagagagc acccacctg cttcggacaa ccctgacata attgccagca 1560  
 cggcagagga ggtggcatcc accagcccag gcattccatca tgcccactgg gtgttggtcc 1620  
 taagaaactg attgattaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680  
 gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740  
 ctgatacctta aaattgctat gctgatagag tggtaggggc tggaagcttg atcaagtctt 1800  
 gtttcttctt gacacagact gattaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln  
 1 5 10 15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val  
 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr  
 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu  
 50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val  
 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys  
 85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser  
 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu  
 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile  
 130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn  
 145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile  
 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

T00T20"CT920550

			180				185				190					
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr	
		195					200					205				
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys	
		210					215					220				
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu	
225					230					235					240	
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe	
				245					250					255		
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val	
			260					265					270			
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr	
		275					280					285				
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys	
		290					295					300				
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr	
305					310					315					320	
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu	
			325					330					335			
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His	
			340					345					350			
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe	
		355					360					365				
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala	
		370					375					380				
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val	
385					390					395					400	
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr	
			405					410					415			
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys	
			420					425					430			
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro	
		435					440					445				
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile	
		450					455					460				

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg 23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc 23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttaciaa aaccttatct 50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctcccgctg cggtcgcgtc gtggcctaga 60  
gatgctgctg ccgcggttgc agttgtcgcg cagcctctg cccgccagcc cgctccaccg 120  
ccgtagcgcg cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180  
tacaggcgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgcctgc 240  
tgagtgcctc ggatttggac ctgagaggag ggcagccagt ctgccgggga gggacacaga 300

ggccttggtta taaagtcatt tactttccatg atactttctcg aagactgaac tttgaggaag 360  
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420  
 agaaactgat agaaaagtgc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480  
 ggctcaggag gcgtgaggag aaacaaaagca atagcacagc ctgccaggac ctttatgctt 540  
 ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcgcca 600  
 gcgaggctcg cgtggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660  
 acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720  
 ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780  
 cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840  
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccctt ctctctctcc 900  
 ttgtgggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960  
 cagaccctag cacaaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020  
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080  
 ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140  
 tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200  
 tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaattg 1260  
 ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320  
 aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380  
 ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440  
 tccccacgac ctctgttgg acccccacgt tttggctgta tcctttatcc cagccagtca 1500  
 tccagctcga ccttatgaga aggtaccttg cccaggtctg gcacatagta gagtctcaat 1560  
 aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620  
 aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680  
 atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740  
 ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800  
 agcaggaaaa aaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
 1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
 20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
 35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
 50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
 65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
 85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
 100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

&lt;210&gt; 138

<211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50  
  
 <210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 139  
 aagccaaaga agcctgcagg aggg 24  
  
 <210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 140  
 cagtccaagc ataaaggtcc tggc 24  
  
 <210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgactcg 240  
 cctgcaccag cggcgggttg ccttggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcgtg ttctgacacg gggctcggag 360  
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc tttcaccaac cttcaaccca caggaggtct ttattcggtc 660  
 cactaacatt tttcgggaatc tggagtccac ccgttgtttg ctggctgggc ttttccagtg 720

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgatatcc 780  
 caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840  
 ttacagcca ggaatctcag aggatttgaa aaagggtgaag gacaggatgg gcattgacag 900  
 tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960  
 cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgacaga gagctgtgga 1020  
 cacatccttg tacatactgc ccaaggaaga cagggaagt cttcagatgg cagtagggcc 1080  
 attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140  
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200  
 gaccctgggg atttttgacc aaaaatggcc accgtttgct gttgacctga ccatggaact 1260  
 ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320  
 ggtgccgaga gggtgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380  
 agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440  
 agttggaat gaagagtaac tgatttataa aagcaggatg tggttgatttt aaaataaagt 1500  
 gcctttatac aatg 1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val  
 1 5 10 15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala  
 20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu  
 35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro  
 50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu  
 65 70 75 80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu  
 85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu  
 100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly  
 115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val  
 130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe  
 145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu  
 165 170 175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

0930345-0100  
 100T20-CT920550



<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatctc agctcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240  
 gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300  
 agctgccagc ggaaccccta gtggtatttt gtatgagcca ccagcagaaa aagagcaaaa 360  
 ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420  
 agaagaagtt tatgattgtt cacatgatga agatgctggg gcacgtgtg agaaccaga 480  
 gagctctttc tccccagtcc cagaggggtg caggctggct gacggccctg ggcattgcaa 540  
 gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600  
 cctccggggc gcaaaggtgg tgtgccggca gctgggatgt gggagggctg tactgactca 660  
 aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720  
 ctcaggacga gaagcaaccc ttcaggattg cccttctggg ccttggggga agaacacctg 780  
 caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840  
 aggagacaac ctctgctctg ggcgactgga ggtgctgcac aaggggcgtat ggggctctgt 900  
 ctgtgatgac aactggggag aaaaggagga ccaggtggta tgcaagcaac tgggctgtgg 960  
 gaagtccctc tctccctcct tcagagaccg gaaatgctat ggccctgggg ttggccgcat 1020  
 ctggctggat aatgttcgtt gctcagggga ggagcagtcc ctggagcagt gccagcacag 1080  
 attttggggg tttcacgact gcaccacca ggaagatgtg gctgtcatct gctcagtgtg 1140  
 ggtgggcatc atctaacttg ttgagtgcct gaatagaaga aaaacacaga agaagggagc 1200  
 atttactgtc tacatgactg catgggatga acactgatct tcttctgccc ttggactggg 1260  
 acttatactt ggtgcccctg attctcaggc cttcagagtt ggatcagaac ttacaacatc 1320  
 aggtctagtt ctcaggccat cagacatagt ttggaactac atcaccacct ttcctatgtc 1380  
 tccacattgc acacagcaga ttcccagcct ccataattgt gtgtatcaac tacttaaata 1440  
 cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccatttgtcc 1500  
 tgtttctctg aagaactctg acaaaatata gattttggta ctgaaagaga ttctagagga 1560  
 acggaatttt aaggataaat tttctgaatt ggttatgggg tttctgaaat tggctctata 1620  
 atctaattag atataaaatt ctggttaactt tatttacaat aataaagata gcactatgtg 1680  
 ttcaaa 1686

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
 1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
 20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
 35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
 50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
 65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
 85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
 100 105 110

```
<210> 149
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
```

## oligonucleotide probe

&lt;400&gt; 149

ttcagctcat caccttcacc tgcc

24

&lt;210&gt; 150

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 150

ggctcataca aaataccact aggg

24

&lt;210&gt; 151

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

&lt;210&gt; 152

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

actgcaactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctgcacctcg 60  
 acccacgcgt ccgcggacgc gtgggacggac gcgtgggccc gctaccagga agagtctgcc 120  
 gaaggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180  
 cctgggcgtc ttcggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240  
 gaatgctgtg gtggtgatca caggcgccac ctcagggtg ggcaaagaat gtgcaaaagt 300  
 cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360  
 gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420  
 ggtgaccttc gacctcacag actctggggc catagtgtga gcagcagctg agatcctgca 480  
 gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540  
 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600  
 tgcctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660  
 catcagcagc atccagggga agatgagcat tccttttcga tcagcatatg cagcctccaa 720  
 gcacgcaacc caggctttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780  
 ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaatg ccatcaccgc 840  
 ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900  
 ggtggccccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960  
 cttactgcct tccttggtg tttatcttcg aactctggct cctgggctct tcttcagcct 1020  
 catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

```

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1260
ggaaacactt aaggaataaa tatggagctg ggggtttaaca ctaaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttgcccgcc atggcccaac ttgtttattg cagcttataa tggttac 1427

```

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1              5              10              15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
      20              25              30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
      35              40              45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
      50              55              60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
      65              70              75              80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
      85              90              95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
      100             105             110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
      115             120             125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
      130             135             140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
      145             150             155             160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
      165             170             175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
      180             185             190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
      195             200             205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

```

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235 240
Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
	245	250 255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val		
	260	265 270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
	275	280 285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
	290	295 300
Arg Lys Ser Lys Asn Ser		
305	310	

&lt;210&gt; 154

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 154

ggtgctaaac tggtgctctg tggc

24

&lt;210&gt; 155

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 155

cagggcaaga tgagcattcc

20

&lt;210&gt; 156

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 156  
tcatactgtt ccatctcggc acgc

24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatggtgggg ccctagaaga gctcatcaga gaactcacgg cttctcatgc

50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
cccacgcgtc cgctggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
aaaaaaaaaa acacacccaaa cgctcgagc caaaaaggg atgaaatttc ttctggacat 120  
cctcctgctt ctcccgttac tgatcgctctg ctccctagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240  
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaaacagc tgccaaatgc aaggggactgg gtgccaagggt 360  
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaagggt 420  
gaaggcagaa attggagatg ttagtatttt agtaaataat gctggtgtag tctatacatc 480  
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540  
acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660  
aagcaagttt gctgctgttg gatctcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780  
aaatccaagt acaagtttgg gaccactctt ggaacctgag gaagtggtaa acaggctgat 840  
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900  
aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtgt 960  
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020  
aactgattta ccagggttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080  
cttctgtttt ttctaattat cccattttct tcaatatcat ttttgaggct ttggcagtct 1140  
tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200  
tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac tttattaaaa 1260  
taattttcaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320  
ttatttaaca tatattttta tttttgattg cacttaaatt ttgtataatt tgtgtttctt 1380  
ttttgtttct acataaaatc agaaacttca agctctctaa ataaaatgaa ggactatatc 1440  
tagtgggtatt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctacccatt 1500  
gccactctgt ttcttgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560  
gctagaggtg gatacacgtg ttgcaagtga aaaagcatca ctgggattta aggagaattg 1620  
agagaatgta ccacaaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771

<210> 159

2025-07-04 15:05:00

<212> PRT

<400> 159

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys  
20 25 30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile  
35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val  
50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys  
65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn  
85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly  
100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp  
115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn  
130 135 140

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
145					150					155					160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His  
165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala  
180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile  
195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly  
210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu  
225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met  
245 250 255



Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
                   260                                  265                                  270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
                   275                                  280                                  285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
                   290                                  295                                  300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg 23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 161

atcccatgca tcagcctgtt tacc 24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag 48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60  
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120

attgtttcgc tggctcctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180  
 agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct caccctttac 240  
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggctcggccc tttcccagga 300  
 ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360  
 ttctttctggt tcttcccagc tcagatacag ccagaagatg ccccgtagt tctctggcta 420  
 caggggtgggc cgggaggttc atccatgttt ggactctttg tggaacatgg gccttatgtt 480  
 gtcacaagta acatgacctt gcgtgacaga gacttccctt ggaccacaac gctctccatg 540  
 cttttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600  
 gcagtcaatg aggacgatgt agcacgggat ttatacagt cactaattca gtttttccag 660  
 atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720  
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
 aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840  
 tatgcagaat tcctgtacca aattggcttg ttggatgaga agcaaaaaaa gtacttccag 900  
 aagcagtgcc atgaatgcat agaacacatc aggaagcaga actgggttga ggcttttgaa 960  
 atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020  
 acaggatgta gtaattacta taactttttg cgggtgcacgg aacctgagga tcagctttac 1080  
 tatgtgaaat ttttgtcact cccagaggtg agacaagcca tccacgtggg gaatcagact 1140  
 tttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaag 1200  
 ccatgggttaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260  
 atcatcgtgg cagctgccct gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320  
 caggaataca agaaggcaga aaaaaaagtt tggagatct ttaaactctga cagtgaagtg 1380  
 gctgggttaca tccggcaagc ggggtgacttc catcaggtaa ttattcgagg tggaggacat 1440  
 attttaccct atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500  
 aaaggatggg atccttatgt tggataaact accttcccaa aagagaacat cagaggtttt 1560  
 cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620  
 tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680  
 ttttgggggg agatgtttac tacaaaatta acatgagtag atgagtaaga attacattat 1740  
 ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800  
 ttttagggtc ttgaatagga agtttttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860  
 taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920  
 gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980  
 ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040  
 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65					70						75				80
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85					90					95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
		115					120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150					155					160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165					170					175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225					230					235					240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245					250					255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260					265					270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
		275					280					285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325					330					335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165

ttccatgccca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

0903645-04001

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

aqctctcaga ggctgggtcat aggg

24

<211> 50

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

<211> 2477

<212> DNA

<213> Homo sapiens

cgagggcttt	tccggtccg	gaatggcaca	tgtgggaatc	ccagtcttgt	tggctacaac	60
atttttccct	ttcctaacaa	gttctaacag	ctgttctaac	agctagtgat	cagggggttct	120
tcttgctgga	gaagaaaggg	ctgagggcag	agcagggcac	tctcactcag	ggtgaccagc	180
tccttgccctc	tctgtggata	acagagcatg	agaaagtgaa	gagatgcagc	ggagtgaggt	240
gatggaagtc	taaaatagga	aggaattttg	tgtgcaatat	cagactctgg	gagcagttga	300
cctggagagc	ctgggggagg	gcctgcctaa	caagctttca	aaaaacagga	gcgacttcca	360
ctgggctggg	ataagacgtg	ccggtaggat	agggaaagact	gggttttagtc	ctaatatcaa	420
attgactggc	tgggtgaact	tcaacagcct	tttaacctct	ctgggagatg	aaaacgatgg	480
cttaaggggc	cagaaataga	gatgctttgt	aaaataaaaat	tttaaaaaaa	gcaagtattt	540
tatagcataa	aggctagaga	ccaaaataga	taacaggatt	ccctgaacat	tcctaagagc	600
gagaaagtat	gttaaaaata	gaaaaaccaa	aatgcagaag	gaggagactc	acagagctaa	660
accaggatgg	ggaccctggg	tcaggccagc	ctctttgtctc	ctcccggaaa	ttatttttgg	720
tctgaccact	ctgccttgtg	ttttgcagaa	tcatgtgagg	gccaaaccggg	gaaggtggag	780
cagatgagca	cacacaggag	ccgtctcctc	accgcgcgcc	ctctcagcat	ggaacagagg	840
cagccctggc	cccgggccct	ggaggtggac	agccgctctg	tggctctgct	ctcagtggtc	900
tgggtgctgc	tggccccccc	agcagccggc	atgcctcagt	tcagcacctt	ccactctgag	960
aatcgtgact	ggaccttcaa	ccacttgacc	gtccaccaag	ggacgggggc	cgtctatgtg	1020
ggggccatca	accgggtcta	taagctgaca	ggcaacctga	ccatccaggt	ggctcataag	1080
acagggccag	aagaggacaa	caagtctcgt	taccgcgcc	tcatcgtgca	gccttgacgc	1140
gaagtgtca	ccctcaccaa	caatgtcaac	aagctgctca	tcattgacta	ctctgagaac	1200
cgctgtctgg	cctgtgggag	cctctaccag	ggggtctgca	agctgctgcg	gctggatgac	1260
ctcttcatcc	tgggtggagc	atcccacaag	aaggagcact	acctgtccag	tgtcaacaag	1320
acgggcacca	tgtacggggt	gattgtgcgc	tctgaggggtg	aggatggcaa	gctcttcac	1380
ggcacggctg	tggatgggaa	gcaggattac	ttcccgacc	tgtccagccg	gaagctgcgc	1440
cgagaccctg	agtcttcagc	catgctcgac	tatgagctac	acagcgattt	tgtctcctct	1500
ctcatcaaga	tcctctcaga	caccctggcc	ctggctctcc	actttgacat	cttctacatc	1560
tacggctttg	ctagtggggg	ctttgtctac	tttctcactg	tccagcccca	gacccctgag	1620
qqtgtqccca	tcaactccgc	tggagacctc	ttctacacct	cacgcacgtg	gcggctctgc	1680

```

aaggatgacc ccaagttcca ctcatacgtg tccctgccct tcggctgcac ccggggccggg 1740
gtggaatacc gcctcctgca ggctgcttac ctggccaagc ctggggactc actggcccag 1800
gccttcaata tcaccagcca ggacgatgta ctctttgcca tcttctccaa agggcagaag 1860
cagtatcacc acccgcccga tgactctgcc ctgtgtgcct tccctatccg ggccatcaac 1920
ttgcagatca aggagcgctt gcagtcctgc taccagggcg agggcaacct ggagctcaac 1980
tggctgctgg ggaaggacgt ccagtgcacg aaggcgcttg tccccatcga tgataacttc 2040
tgtggactgg acatcaacca gcccctggga ggctcaactc cagtggaggg cctgaccctg 2100
tacaccacca gcagggaccg catgacctct gtggcctcct acgtttacaa cggctacagc 2160
gtgggtttttg tggggactaa gagtggcaag ctgaaaaagg taagagtcta tgagttcaga 2220
tgctccaatg ccattcacct cctcagcaaa gagtccctct tggaaggtag ctattggttg 2280
agatttaact ataggcaact ttattttctt gggaacaaa ggtgaaatgg ggaggtaaga 2340
aggggttaat tttgtgactt agcttctagc tacttcctcc agccatcagt cattgggtat 2400
gtaaggaatg caagcgtatt tcaatatttc ccaaacttta agaaaaaact ttaagaagg 2460
acatctgcaa aagcaaa 2477

```

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

```

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
  1              5              10              15

```

```

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
      20              25              30

```

```

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35              40              45

```

```

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50              55              60

```

```

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
      65              70              75              80

```

```

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85              90              95

```

```

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100             105             110

```

```

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
      115             120             125

```

```

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
      130             135             140

```

```

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
      145             150             155             160

```

```

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
      165             170             175

```

Glu	Asn	Arg	Leu	Leu	Ala	Cys	Gly	Ser	Leu	Tyr	Gln	Gly	Val	Cys	Lys
			180				185						190		
Leu	Leu	Arg	Leu	Asp	Asp	Leu	Phe	Ile	Leu	Val	Glu	Pro	Ser	His	Lys
			195				200				205				
Lys	Glu	His	Tyr	Leu	Ser	Ser	Val	Asn	Lys	Thr	Gly	Thr	Met	Tyr	Gly
			210				215			220					
Val	Ile	Val	Arg	Ser	Glu	Gly	Glu	Asp	Gly	Lys	Leu	Phe	Ile	Gly	Thr
225				230						235			240		
Ala	Val	Asp	Gly	Lys	Gln	Asp	Tyr	Phe	Pro	Thr	Leu	Ser	Ser	Arg	Lys
			245						250			255			
Leu	Pro	Arg	Asp	Pro	Glu	Ser	Ser	Ala	Met	Leu	Asp	Tyr	Glu	Leu	His
			260			265						270			
Ser	Asp	Phe	Val	Ser	Ser	Leu	Ile	Lys	Ile	Pro	Ser	Asp	Thr	Leu	Ala
			275			280						285			
Leu	Val	Ser	His	Phe	Asp	Ile	Phe	Tyr	Ile	Tyr	Gly	Phe	Ala	Ser	Gly
			290			295			300						
Gly	Phe	Val	Tyr	Phe	Leu	Thr	Val	Gln	Pro	Glu	Thr	Pro	Glu	Gly	Val
305				310						315			320		
Ala	Ile	Asn	Ser	Ala	Gly	Asp	Leu	Phe	Tyr	Thr	Ser	Arg	Ile	Val	Arg
			325						330			335			
Leu	Cys	Lys	Asp	Asp	Pro	Lys	Phe	His	Ser	Tyr	Val	Ser	Leu	Pro	Phe
			340			345						350			
Gly	Cys	Thr	Arg	Ala	Gly	Val	Glu	Tyr	Arg	Leu	Leu	Gln	Ala	Ala	Tyr
			355			360						365			
Leu	Ala	Lys	Pro	Gly	Asp	Ser	Leu	Ala	Gln	Ala	Phe	Asn	Ile	Thr	Ser
			370			375			380						
Gln	Asp	Asp	Val	Leu	Phe	Ala	Ile	Phe	Ser	Lys	Gly	Gln	Lys	Gln	Tyr
385				390						395			400		
His	His	Pro	Pro	Asp	Asp	Ser	Ala	Leu	Cys	Ala	Phe	Pro	Ile	Arg	Ala
			405			410						415			
Ile	Asn	Leu	Gln	Ile	Lys	Glu	Arg	Leu	Gln	Ser	Cys	Tyr	Gln	Gly	Glu
			420			425						430			
Gly	Asn	Leu	Glu	Leu	Asn	Trp	Leu	Leu	Gly	Lys	Asp	Val	Gln	Cys	Thr
			435			440						445			
Lys	Ala	Pro	Val	Pro	Ile	Asp	Asp	Asn	Phe	Cys	Gly	Leu	Asp	Ile	Asn

450                      455                      460  
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
 465                      470                      475                      480  
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
                     485                      490                      495  
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
                     500                      505                      510  
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
                     515                      520                      525  
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
                     530                      535                      540  
 Leu Tyr Phe Leu Gly Glu Gln Arg  
 545                      550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

tggaataccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



<400> 173  
ggactcactg gccagggcct tcaatatcac cagccaggac gat

42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
aggctcccgc gcgcggctga gtgcggactg gagtgggaac ccgggtcccc gcgcttagag 60  
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
tgctggctcgt cttgggcttc ctgggtgctcc gcaggctgga ctggagcacc ctggccctc 180  
tgccggtccg ccacgcacag ctggggctgc aggccaaagg ctggaacttc atgctggagg 240  
attccacctt ctggatcttc gggggctcca tccactattt ccgtgtgccc agggagtact 300  
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360  
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420  
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggcccc 480  
acatctgcag tgagatggac ctccggggct tgcccagctg gctactccaa gacctggca 540  
tgaggctgag gacaacttac aagggttca ccgaagcagt ggacctttat ttgaccacc 600  
tgatgtccag ggtggtgcc ctccagtaca agcgtggggg acctatcatt gcctgcagg 660  
tgagagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
cactggagga ccgtggcatt gtggaactgc tctgacttc agacaacaag gatgggctga 780  
gcaaggggat tgtccagga gtcttgcca ccatcaactt gcagtcaaca cacgagctgc 840  
agctactgac cacttttctc ttcaacgtcc aggggactca gcccaagatg gtgatggagt 900  
actggacggg gtggtttgac tcgtggggag gccctcacia tatcttgat tcttctgagg 960  
ttttgaaaac cgtgtctgcc attgtggacg ccggctcctc catcaacctc tacatgttcc 1020  
acggaggcac caactttggc ttcatgaatg gagccatgca ctccatgac tacaagtcag 1080  
atgtcaccag ctatgactat gatgctgtgc tgacagaagc cggcgattac acggccaagt 1140  
acatgaagct tcgagacttc ttccgctcca tctcaggcat cctctcctc ccccccactg 1200  
accttcttcc caagatgccg tatgagccct taacgccagt cttgtacctg tctctgtggg 1260  
acgccctcaa gtacctgggg gagccaatca agtctgaaaa gcccatcaac atggagaacc 1320  
tgccagtcaa tgggggaaat ggacagtcct tcgggtacat tctctatgag accagcatca 1380  
cctcgtctgg catcctcagt ggccacgtgc atgatcgggg gcagggtgtt gtgaacacag 1440  
tatccatagg attcttggac tacaagacaa cgaagattgc tgtccccctg atccagggtt 1500  
acaccgtgct gaggatcttg gtggagaatc gtgggcgagt caactatggg gagaatattg 1560  
atgaccagcg caaaggctta attggaaatc tctatctgaa tgattcacc ctgaaaaact 1620  
tcagaatcta tagcctggat atgaagaaga gcttctttca gaggttcggc ctggacaaat 1680  
ggngttccct ccagaaaca ccacattac ctgctttctt cttgggtagc ttgtccatca 1740  
gtccacgcc ttgtgacacc tttctgaagc tggagggtcg ggagaagggg gttgtattca 1800  
tcaatggcca gaaccttga cgttactgga acattggacc ccagaagacg ctttacctcc 1860  
caggtccctg gttgagcagc ggaatcaacc aggtcatcgt ttttgaggag acgatggcgg 1920  
gccctgcatt acagttcacg gaaaccccc accctggcag gaaccagtac attaagtga 1980  
cggtggcacc cctcctgct ggtgccagtg ggagactgcc gcctcctctt gacctgaagc 2040  
ctgggtggctg ctgccccacc cctcactgca aaagcatctc cttaagtagc aacctcaggg 2100  
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaagggtg 2160  
ggatggctct gggcctggct ttgttgatga tggctttcct acagccctgc tcttgtgccg 2220  
aggctgtcgg gctgtctcta ggggtggagc agctaatac atcgcccagc ctttggccct 2280

cagaaaaagt gctgaaacgt gcccttgcac cggacgtcac agccctgcga gcctctgctg 2340  
 gactcaggcg tgctctttgc tggttcctgg gaggcttggc cacatccctc atggcccat 2400  
 tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc 2460  
 tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa 2520  
 ctcggcgtga gaaacatgtg acttccccctt tcccttccca ctgctgctt cccacagggt 2580  
 gacaggctgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcaggtgt 2640  
 ctctggtgtt cagtgaggag gacatgtgag tcctggcaga agccatggcc catgtctgca 2700  
 catccaggga ggaggacaga aggcccagct cacatgtgag tcctggcaga agccatggcc 2760  
 catgtctgca catccaggga ggaggacaga aggcccagct cacatgtgag tcctggcaga 2820  
 agccatggcc catgtctgca catccaggga ggaggacaga aggcccagct cacatgtgag 2880  
 tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga aggcccagct 2940  
 cagtggcccc cgctccccac cccccacgcc cgaacagcag gggcagagca gccctccttc 3000  
 gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggcttg 3060  
 ggctcactgt cctgagttgc agtaaagcta taaccttgaa tcacaa 3106

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu  
 1 5 10 15

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp  
 20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln  
 35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe  
 50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp  
 65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr  
 85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser  
 100 105 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly  
 115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp  
 130 135 140

0903615.01001

Leu 145	Gly	Gly	Leu	Pro	Ser 150	Trp	Leu	Leu	Gln	Asp 155	Pro	Gly	Met	Arg	Leu 160
Arg	Thr	Thr	Tyr	Lys 165	Gly	Phe	Thr	Glu	Ala 170	Val	Asp	Leu	Tyr	Phe	Asp 175
His	Leu	Met	Ser 180	Arg	Val	Val	Pro	Leu 185	Gln	Tyr	Lys	Arg	Gly	Gly	Pro 190
Ile	Ile	Ala 195	Val	Gln	Val	Glu	Asn 200	Glu	Tyr	Gly	Ser	Tyr 205	Asn	Lys	Asp 210
Pro	Ala 210	Tyr	Met	Pro	Tyr	Val 215	Lys	Lys	Ala	Leu	Glu 220	Asp	Arg	Gly	Ile 225
Val 225	Glu	Leu	Leu	Leu	Thr 230	Ser	Asp	Asn	Lys	Asp 235	Gly	Leu	Ser	Lys	Gly 240
Ile	Val	Gln	Gly	Val 245	Leu	Ala	Thr	Ile	Asn 250	Leu	Gln	Ser	Thr	His	Glu 255
Leu	Gln	Leu	Leu 260	Thr	Thr	Phe	Leu	Phe 265	Asn	Val	Gln	Gly	Thr 270	Gln	Pro 275
Lys	Met 275	Val	Met	Glu	Tyr	Trp	Thr 280	Gly	Trp	Phe	Asp	Ser 285	Trp	Gly	Gly 290
Pro	His 290	Asn	Ile	Leu	Asp	Ser 295	Ser	Glu	Val	Leu	Lys 300	Thr	Val	Ser	Ala 305
Ile 305	Val	Asp	Ala	Gly	Ser 310	Ser	Ile	Asn	Leu	Tyr 315	Met	Phe	His	Gly	Gly 320
Thr	Asn	Phe	Gly	Phe 325	Met	Asn	Gly	Ala	Met 330	His	Phe	His	Asp	Tyr 335	Lys 340
Ser	Asp	Val	Thr 340	Ser	Tyr	Asp	Tyr	Asp 345	Ala	Val	Leu	Thr	Glu 350	Ala	Gly 355
Asp	Tyr 355	Thr	Ala	Lys	Tyr	Met	Lys 360	Leu	Arg	Asp	Phe	Phe 365	Gly	Ser	Ile 370
Ser	Gly 370	Ile	Pro	Leu	Pro	Pro 375	Pro	Pro	Asp	Leu	Leu 380	Pro	Lys	Met	Pro 385
Tyr 385	Glu	Pro	Leu	Thr	Pro 390	Val	Leu	Tyr	Leu	Ser 395	Leu	Trp	Asp	Ala	Leu 400
Lys	Tyr	Leu	Gly	Glu 405	Pro	Ile	Lys	Ser	Glu 410	Lys	Pro	Ile	Asn	Met	Glu 415
Asn	Leu	Pro	Val 420	Asn	Gly	Gly	Asn 425	Gly	Gln	Ser	Phe	Gly	Tyr 430	Ile	Leu 435

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60  
ccctggtgag gggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120  
aaggggagca aagccgggct cggcccagg ccccaggac ctccatctcc caatgttggga 180  
ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgct gtaaaccgcca 240  
tggtcccaa gaagctgtcc tgccttcgtt ccctgctgct gccgctcagc ctgacgctac 300  
tgctgccccca ggcagacact cggtcgttcg tagtggatag gggtcagac cggtttctcc 360  
tagacggggc cccgttcgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

tgcctttgggc cgaccggcctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480  
 atgtgccctg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540  
 acctcattgc ctttctgaat gaggcagctc tagcgaacct gttgggtcata ctgagaccag 600  
 gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctgggtg cttcgaaaac 660  
 ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctgggtca 720  
 aggtcttgct gcccaagata tatccatggc tttatcacia tgggggcaac atcattagca 780  
 ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840  
 tggctgggct cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900  
 ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960  
 ctgacaacat gaccaaatac tttaccctgc ttcggaagta tgaaccccat gggccattgg 1020  
 taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacggg 1080  
 ctgtgtcagc tgtaacccaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140  
 tgtacatgtt ccatggaggt accaactttg gatattggaa tgggtgccgat aagaaggagc 1200  
 gcttccttcc gattactacc agctatgact atgatgcacc tatacttgaa gcaggggacc 1260  
 ccacacctaa gctttttgct cttcgagatg tcatcagcaa gttccaggaa gttcctttgg 1320  
 gacctttacc tcccccgagc cccaagatga tgccttggacc tgtgactctg cacctgggtg 1380  
 ggcatttact ggctttccta gacttgcttt gccccgtgg gcccttccat tcaatcttgc 1440  
 caatgacctt tgaggctgtc aagcaggacc atggcttccat gttgtaccga acctatatga 1500  
 cccataccat ttttgagcca acaccattct ggggtgccaa taatggagtc catgaccgtg 1560  
 cctatgtgat ggtggatggg gtgttccagg gtgttgtgga gcgaaatat agagacaaac 1620  
 tatttttgac ggggaaactg ggggtccaaac tggatatctt ggtggagaac atggggaggc 1680  
 tcagctttgg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740  
 aaacaatcct taccagtggt atgatgttcc ctctgaaaat tgataacctt gtgaagtggg 1800  
 ggtttccctt ccagttgcc aatggcccat atcctcaagc tcttcttggc cccacattct 1860  
 actccaaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920  
 ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccggtactgg acaaagcagg 1980  
 ggccacaaca gacctctac gtgccaagat tctgtctgtt tcttagggga gccctcaaca 2040  
 aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtcca tttttggata 2100  
 agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160  
 atacactgag tgccctctgaa ccaatggagt taagtgggca ctgaaaggta ggcggggcat 2220  
 ggtggctcat gctgtaatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280  
 tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340  
 aaattagccc ggcgtgatgg tgggcacctc taatcccagc tacttggggag gctgagggca 2400  
 ggagaattgc ttgaatccag gaggcagagg ttgcagttag tggaggttgt accactgcac 2460  
 tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa 2505

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
 1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
 50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80  
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95  
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110  
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125  
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140  
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160  
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175  
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190  
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205  
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220  
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro  
 225 230 235 240  
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255  
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

	340		345		350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro	355		360		365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu	370		375		380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu	385		390		395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		405		410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		420		425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		435		440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		450		455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		465		470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		485		490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		500		505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		515		520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		530		535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		545		550	555
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		565		570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		580		585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		595		600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		610		615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

090616-0700



<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182  
 tggcaccag aatggtgttg gctc 24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
 gctttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60  
 gcaccacaaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattat 120  
 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagttttag tgacattcca gatgtcaaaa 240  
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300  
 ttggtgtgtt cttgtcagaa gttagtgaat ataaacttag ggaaattagt ttgaacctatg 360  
 agtggacatt tgaaaaactc aggcagcaca ttccacgcaa cgcccaggac aagcaggagt 420  
 tgcattctgt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480  
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540  
 acctccaaga gctccacctc tgccactgcc ctgcaaaagt tgaacagact gcttttagct 600  
 ttcttcgcga tcacttgaga tgcccttcacg tgaagttcac tgatgtggct gaaattcctg 660  
 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840  
 caaagttagt cattcataat gacggcacta aactcttggt actgaacagc cttaagaaaa 900  
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
 ttttcagcct ctctaattta caggaactgg atttaagtc caataacatt cgcacaattg 1020  
 aggaaatcat cagtttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080  
 aaattgttac tattcctccc tctattaccc atgtcaaaaa cttggagtca ctttatttct 1140  
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag ttacagaaa ctcatatgct 1200  
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260  
 tgcagcattt gcatatcact gggaacaaa tggacattct gccaaaacaa ttgttttaaat 1320

gcataaaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380  
 ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440  
 cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttggttg gaagatcacc 1500  
 tttttgatac cctgccactc gaagtcaaag aggcattgaa tcaagacata aatattccct 1560  
 ttgcaaattg gatttaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620  
 agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680  
 cttttaaaat aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740  
 aatgtttgta ggggttttaag tcattcattt ccaaattcatt tttttttttc ttttggggaa 1800  
 aggggaaggaa aaattataat cactaatctt ggttcttttt aaattgtttg taacttggat 1860  
 gctgccgcta ctgaatgttt acaaattgct tgctgctaa agtaaattgat taaattgaca 1920  
 ttttcttact aaaaaaaaaa aaaaaaa 1947

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile  
 1 5 10 15

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg  
 20 25 30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser  
 35 40 45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His  
 50 55 60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe  
 65 70 75 80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His  
 85 90 95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln  
 100 105 110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala  
 115 120 125

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro  
 130 135 140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu  
 145 150 155 160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser  
 165 170 175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val  
 180 185 190

090351.001

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465                      470                      475                      480  
 Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro  
                          485                      490                      495  
 Phe Ala Asn Gly Ile  
                          500

<210> 186  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                          oligonucleotide probe

<400> 186  
 cctccctcta ttacccatgt c                      21

<210> 187  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                          oligonucleotide probe

<400> 187  
 gaccaacttt ctctgggagt gagg                      24

<210> 188  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                          oligonucleotide probe

<400> 188  
 gtcactttat ttctctaaca acaagctcga atccttacca gtggcag                      47

<210> 189  
 <211> 2917  
 <212> DNA  
 <213> Homo sapiens

<400> 189  
 cccacgcgtc cggccttctc tctggacttt gcatttccat tccttttcat tgacaaactg 60  
 acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccctggg 120  
 aagacatttg tgttttacac acataaggat ctgtgtttgg ggtttcttct tcctccctg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240  
gcacttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300  
atcgctggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtcctttac 360  
ttcaaaatac acaacgcgct aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420  
cacaacccag acaaggtgtg gtgggccaag aacagccagg ccaaaacccat tgccacggag 480  
tcttgtcctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540  
ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaaa 600  
gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660  
agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720  
cagctgctgg agatccctac agagagcttc cactgggggc aacccttcca ggaaggagtt 780  
ggggagagag aaccctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840  
ctcacacaaa tctacccctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900  
gctgatgtaa cacagagcct ataaaagctg tcggtcctta aggctgccc aagccttgcc 960  
aaaatggagc ttgtaagaag gctcatgcca ttgacctct taattctctc ctggttgccg 1020  
gagctgacaa tggcggaggc tgaaggcaat gcaagctgca cagtcagtct aggggggtgc 1080  
aatatggcag agaccacaa agccatgatc ctgcaactca atcccagtg gaactgcacc 1140  
tggacaatat aaagaccaga aaacaaaagc atcagaatta tcttttctta tgtccagctt 1200  
gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac ctccagcaat 1260  
gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttctgtatt tgaatcatca 1320  
tccagtacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtcttt 1380  
gtcttctact acttcttctc tctaacatc tctattccaa actgtggcgg ttacctggat 1440  
accttggaag gatccttcac cagccccaat taccacaaag cgcacctga gctggcttat 1500  
tgtgtgtggc acatacaagt ggagaaagat tacaagataa aactaaactt caaagagatt 1560  
ttcctagaaa tagacaaaca gtgcaaattt gatcttcttg ccatctatga tggccccctc 1620  
accaactctg gcctgattgg acaagtctgt ggccgtgtga ctcccacctt cgaatcgtca 1680  
tcaaactctc tgactgtcgt gttgtctaca gattatgcca attcttaccg gggattttct 1740  
gcttctaca cctcaattta tgcagaaaac atcaacacta catctttaac ttgctcttct 1800  
gacaggatga gagttattat aagcaaacc tacctagagg cttttaactc taatgggaat 1860  
aacttgcaac taaaagaccc aacttgca ccaaaattat caaatgtgt ggaattttct 1920  
gtccctctta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980  
aatataatca ccttttctgc atcctcaact tctgaagtga tcaccctca gaaacaaactc 2040  
cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100  
gaagatgatg taatacaaa tcaaaatgca ctgggcaaat ataacaccag catggctctt 2160  
tttgaatcca attcatttga aaagactata cttgaatcac catattatgt ggatttgaac 2220  
caaactcttt ttgttcaagt tagtctgcac acctcagatc caaatttggg ggtgttctt 2280  
gatacctgta gagcctctcc cactctgac tttgcatctc caacctacga cctaatacaag 2340  
agtggatgta gtcgagatga aacttgtaag gtgtatccct tatttggaca ctatgggaga 2400  
ttccagttta atgcctttta attcttgaga agtatgagct ctgtgtatct gcagtgtaaa 2460  
gttttgatat gtgatagcag tgaccaccag tctcgctgca atcaagggtt tgtctccaga 2520  
agcaaacgag acatttcttc atataaatgg aaacagatt ccatcatagg acccattcgt 2580  
ctgaaaaggg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgcggaa 2640  
gaaactccaa accagccttt caacagtgtg catctgtttt ccttcattgg tctagctctg 2700  
aatgtggtga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760  
aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgtttc 2820  
tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880  
ggcctgaaag tgacacacag gccctgcatgt aaaaaa 2917

&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15  
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30  
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45  
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60  
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80  
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95  
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110  
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125  
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140  
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160  
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175  
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190  
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205  
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220  
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240  
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255  
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270  
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

095025LE-071001  
 T00T20"ET920560

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300  
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350  
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365  
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430  
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445  
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

09072616 07004  
 T00749 "5720660

565                      570                      575  
 Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe  
                     580                      585                      590  
 Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr  
                     595                      600                      605

<210> 191  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                     oligonucleotide probe

<400> 191  
 tctctattcc aaactgtggc g 21

<210> 192  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                     oligonucleotide probe

<400> 192  
 tttgatgacg attcgaaggt gg 22

<210> 193  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                     oligonucleotide probe

<400> 193  
 ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194  
 <211> 2362  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
 gacggaagaa cagcgctccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60  
 cgggacatgc ggccccagga gtcgccagc ctcgcgttcc cggtgctgct gttgctgttg 120  
 ctgctgctgc cgccgccgcc gtgccctgcc cacagcgcca cgcgcttcga cccacactgg 180



gagtccctgg acgccccgcca gctgcccgcg tggtttgacc aggccaaagt cggcatcttc 240  
 atccactggg gagtggttttc cgtgcccagc ttcggtagcg agtggttctg gtggtattgg 300  
 caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagtttc 360  
 aaatatgaag attttggacc actatttaca gcaaaatttt ttaatgccaa ccagtgggca 420  
 gatatttttc aggcctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480  
 tttaccttgt gggggctcaga atattcgtgg aactggaatg ccatagatga gggggccaag 540  
 agggacattg tcaaggaact tgaggtagcc attaggaaca gaactgacct gcgttttgga 600  
 ctgtactatt ccctttttga atggtttcat ccgctcttcc ttgaggatga atccagttca 660  
 ttccataagc ggcaatttcc agtttctaag acattgccag agctctatga gttagtgaac 720  
 aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcacggga tcaatactgg 780  
 aacagcacag gcttcttggc ctggttatat aatgaaagcc cagttcgggg cacagtagtc 840  
 accaatgatc gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900  
 gatcggtata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960  
 aaactgtcct ggggctatag gagggaagct ggaatctctg actatcttac aattgaagaa 1020  
 ttggtgaagc aacttgtaga gacagtttca tgtggaggaa atcttttgat gaattattggg 1080  
 cccacactag atggcaccat ttctgtagtt tttgaggagc gactgaggca agtgggggtcc 1140  
 tggctaaaaa tcaatggaga agctatttat gaaacctata cctggcgatc ccagaatgac 1200  
 actgtcacc cagatgtgtg gtacacatcc aagcctaaag aaaaattagt ctatgccatt 1260  
 tttcttaaat ggccacatc aggacagctg ttccttggcc atcccaaagc tattctgggg 1320  
 gcaacagagg tgaaactact gggccatgga cagccactta actggatttc tttggagcaa 1380  
 aatggcatta tggtagaact gccacagcta accattcatc agatgccgtg taaatggggc 1440  
 tgggctctag ccctaactaa tgtgatctaa agtgacagc agtggtgat gctgcaagtt 1500  
 atgtctaagg ctaggaacta tcaggtgtct ataattgtag cacatggaga aagcaatgta 1560  
 aactggataa gaaaattatt tggcagttca gccctttccc tttttcccac taaatttttc 1620  
 tttaaattacc catgtaacca ttttaactct ccagtgcact ttgccattaa agtctcttca 1680  
 cattgatttg tttccatgtg tgactcagag gtgagaatth tttcacatta tagtagcaag 1740  
 gaattggtgg tattatggac cgaactgaaa attttatgtt gaagccatat ccccatgat 1800  
 tatatagtta tgcatactt aatatgggga tttttcttgg gaaatgcatt gctagtcaat 1860  
 ttttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920  
 cacaccta at gtgtatggta tagactgttg ctcttaggct acagacatat acagcatgtt 1980  
 actgaatact gtaggcaata gtaacagtgg tatttgtata tcgaaacata tggaaacata 2040  
 gagaaggtag agtaaaaata ctgtaaaata aatggtgcac ctgtataggg cacttaccac 2100  
 gaatggagct tacaggactg gaagtgtctc tgggtgagtc agtgagtga tgtgaaggcc 2160  
 taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220  
 ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280  
 caaacgtttt aatttttaaa accttttttg ctcttttgta ataacaacta gcttaaaaca 2340  
 taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met	Arg	Pro	Gln	Glu	Leu	Pro	Arg	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu
1					5				10					15	
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Pro	Pro	Cys	Pro	Ala	His	Ser	Ala	Thr
				20				25					30		
Arg	Phe	Asp	Pro	Thr	Trp	Glu	Ser	Leu	Asp	Ala	Arg	Gln	Leu	Pro	Ala
			35				40					45			



<210> 198

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 198

aacttgcagc atcagccact ctgc

24

<210> 199

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 199

ttccgtgccc agcttcggta gcgagtgggt ctggtggtat tggca

45

<210> 200

<211> 2372

<212> DNA

<213> Homo sapiens

<400> 200

```

agcagggaaa tccggatgtc tcggttatga agtggagcag tgagtgtgag cctcaacata 60
gttcacagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120
catctgaggt gtttcccttg ctctgaaggg gtaggcacga tggccagggtg cttcagcctg 180
gtgttgcttc tcacttccat ctggaccacg aggtccctgg tccaaggctc tttgctgca 240
gaagagcttt ccatccagggt gtcattgcaga attatgggga tcacccttgt gagcaaaaag 300
gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360
ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420
ggctgggttg gagatggatt cgtggtcac tctaggatta gcccaaacc caagtgtggg 480
aaaaatgggg tgggtgtcct gatttggag gtccagtgga gccgacagtt tgcagcctat 540
tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa 600
gatcccatat tcaaacactca aactgcaaca caaacaacag aatttattgt cagtgcagct 660
acctactcgg tggcatcccc ttactctaca atacctgcc ctactactac tctcctgct 720
ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780
gaaactagca ccatgtctac agaaactgaa ccatttgttg aaaataaagc agcattcaag 840
aatgaagctg ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctcctctc 900
tttggtgctg cagctggtct tggattttgc tatgtcaaaa ggtatgtgaa ggccttcct 960
tttacaacaa agaatcagca gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020
gccaatgata gcaaccctaa tgaggaatca aagaaaactg ataaaaacc agaagagtc 1080
aagagtcgaa gcaaaactac cgtgcgatgc ctggaagctg aagtttagat gagacagaaa 1140
tgaggagaca cacctgaggtc tggtttcttt catgctcctt accctgcccc agctggggaa 1200
atcaaaaggg ccaaagaacc aaagaagaaa gtccaccctt ggttcctaac tggaaatcagc 1260
tcaggactgc cattggacta tggagtgcac caaagagaat gcccttctcc ttattgtaac 1320
cctgtctgga tcctatctc ctacctcaa agcttccac ggcttttcta gcctggctat 1380
gtcctaataa tatccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440

```

tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctaggtg gggtgaaagc 1500  
 caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac cctttcttca 1560  
 gctctgaaaag agaaacacgt atcccacctg acatgtcctt ctgagcccgg taagagcaaa 1620  
 agaatggcag aaaagttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680  
 tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacgacag tacactgtca 1740  
 gcagggactg taaacacaga caggggtcaaa gtgttttctc tgaacacatt gagttggaat 1800  
 cactgttttag aacacacaca cttacttttt ctggtctcta ccactgctga ttttttctct 1860  
 aggaaatata cttttacaag taacaaaaat aaaaactcct ataaatttct atttttatct 1920  
 gagttacaga aatgattact aaggaagatt actcagtaat ttgttttaaaa agtaataaaa 1980  
 ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040  
 tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct ggggaagctat 2100  
 ttttttcagt ttgatattt ctagcttatc tacttccaaa ctaattttta tttttgctga 2160  
 gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220  
 atacctaaga agtacattgt tacctctata taccaaagca catttttaaaa gtgccattaa 2280  
 caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340  
 tgtgacaaaa aattaaagca tttagaaaac tt 2372

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr  
 1 5 10 15

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile  
 20 25 30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala  
 35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu  
 50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala  
 65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val  
 85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
 100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys  
 115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile  
 130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence



&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

```

agatggcggt cttggcacct ctaattgctc tcgtgtattc ggtgccgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg cctgtctctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccacccaacg cgaagacggt aaccctgtgtg 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttgataa ttcgcatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaacccc ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagaggggc acttggattg 480
tgagattctt tgccaattgg tctaataact gccaatcatt tgcccctatc tatgctgacc 540
tctcccttaa atacaactgt acaggggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtac aaagttagca catcacccct caccaagcaa ctccctacc 660
tgatcctgtt ccaaggtggc aaggaggcaa tgcggcggcc acagattgac aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaattgagc 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gagcagcctg 840
tggtttcaac ccccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgcttctctc cctgtcaatt ccaggctctt tccataacca caagcctgag 960
gctgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
tctgatttta aagaggcatc tagggaattg tcaggcaccc tacaggaagg cctgccatgc 1080
tgtggccaac tgtttcaact gagcaagaaa gagatctcat aggacggagg gggaaatggt 1140
ttccctccaa gcttggtgca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttgggt 1260
agacctagat ttaaccctaa ggtaagatgc tggggtatag aacgctaaga attttcccc 1320
aaggactctt gcttccctaa gcccttcttg cttcgtttat ggtcttcatt aaaagtataa 1380
gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttgaggga gaaatcccct ggactttcac taacctctg 1560
acatactccc cacaccagtg tgatggcttt ccgtaataaa aagattggga tttccttttg 1620

```

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

```

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
 1              5              10              15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
      20              25              30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
      35              40              45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
      50              55              60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
      65              70              75              80

```



```
<210> 208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 208
gcttggatat tcgcatgggc ctac
```

<400> 212						
ggacagctcg	cggcccccga	gagctctagc	cgtcgaggag	ctgcctgggg	acgtttgccc	60
tggggcccca	gcctggcccc	ggtcaccctg	gcattgaggag	atgggcctgt	tgtccctggg	120
cccattgctc	ctgctgcccc	gctcctacgg	actgcccttc	tacaacggct	tctactactc	180
caacagcgcc	aacgaccaga	acctaggcaa	cggtcatggc	aaagacctcc	ttaatggagt	240
gaagctggtg	gtggagacac	ccgaggagac	cctgttcacc	taccaagggg	ccagtgtgat	300
cctgccttgc	cgctaccgct	acgagccggc	cctggctctc	ccgcggcgtg	tgcgtgtcaa	360
atggtggaag	ctgtcggaga	actggggccc	agagaaggac	gtgctggtgg	ccatcgggct	420
gaggcaccgc	tccctttggg	actaccaagg	cgcgtgcac	ctgcggcagg	acaaagagca	480
tgacgtctcg	ctggagatcc	aggatctgcg	cctggaggac	tatgggcgtt	accgctgtga	540
ggtcattgac	gggctggagg	atgaaagcgg	tctgggtggg	ctggagctgc	gggggtgtgg	600

ctttccttac cagtccccca acgggcgcta ccagttcaac ttccacgagg gccagcaggt 660  
 ctgtgcagag caggctgcgg tgggtggctc ctttgagcag ctcttcgagg cctgggagga 720  
 gggcctggac tggtgcaacg cgggctggct gcaggatgct acgggtgcagt accccatcat 780  
 gttgccccgg cagccctgcg gtggcccagg cctggcacct ggcgtgcgaa gctacggccc 840  
 ccgccaccgc cgctgcacc gctatgatgt attctgcttc gctactgccc tcaaggggcg 900  
 ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaaggg aggcctgcca 960  
 ggaagatgat gccacgatcg ccaaggtggg acagctcttt gccgcctgga agttccatgg 1020  
 cctggaccgc tgcgacgctg gctggctggc agatggcagc gtccgctacc ctgtggttca 1080  
 cccgcatact aactgtgggc cccagagacc tggggtccga agctttggct tccccgacct 1140  
 gcagagccgc ttgtacgggtg tttactgcta ccgccagcac taggacctgg ggcctcccc 1200  
 tgccgcattc cctcactggc tgtgtattta ttgagtgggt cgttttccct tgtgggttg 1260  
 agccatttta actgttttta tacttctcaa tttaaatttt ctttaaacat tttttacta 1320  
 ttttttghaa agcaaacaga acccaatgcc tccctttgct cctggatgcc ccactccagg 1380  
 aatcatgctt gctcccctgg gccatttgcg gttttgtggg cttctggagg gttccccgcc 1440  
 atccaggctg gtctccctcc ctttaaggagg ttggtgcca gaggggcggt tggcctgtct 1500  
 agaatgccgc cgggagtcgg ggcaggtgg gcacagttct ccctgcccct cagcctgggg 1560  
 gaagaagagg gcctcggggg cctccggagc tgggctttgg gcctctctg cccacctcta 1620  
 cttctctgtg aagccgctga cccagtcctg cccactgagg ggctaggggt ggaagccagt 1680  
 tctaggcttc caggcgaat ctgagggaag gaagaaactc ccctccccgt tccccctccc 1740  
 ctctcggttc caaagaatct gttttgttgt catttgtttc tctgtttcc ctgtgtggg 1800  
 aggggccctc aggtgtgtgt actttggaca ataatgggtg ctatgactgc cttccgcca 1860  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980  
 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr  
 1 5 10 15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp  
 20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
 35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
 50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
 65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
 85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
 100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

```
<210> 214
<211> 18
<212> DNA
<213> Artificial Sequence
```

$\langle 220 \rangle$

<400> 214  
tgcttcgcta ctgccctc 18

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 215  
ttcccttgtg ggttggag 18

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

```
<400> 216
agggctggaa gccagttc 18
```

```
<210> 217
<211> 18
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

<400> 217  
agccagtgag gaaatgcg 18

```
<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

<400> 218  
tgtccaaagt acacacacct gagg 24

<210> 219

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 219

gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220

<211> 1503

<212> DNA

<213> Homo sapiens

<400> 220

```

ggagagcggg gccaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60
gcttctgttg ctactgaggg acggggccca ggggaagcca tcccagacg caggccctca 120
tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctcccatg atgacgcca 180
cgggaaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240
ccaactcacc ccagaggaaa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300
cgcgggggac ggcgacggct ggggtgtcgt ggccgagctt cgcgcgtgga tcgcgcacac 360
gcagcagcgg cacatacggg actcgggtgag cgcggcctgg gacacgtacg acacggaccg 420
cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccg 480
tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctggggacga 540
gcggcgcttc cgggtggcgg accaggatgg ggactcgatg gccactcgag aggagctgac 600
agccttctctg caccgcgagg agttccctca catgcgggac atcgtgattg ctgaaaccct 660
ggaggacctg gacagaaaaca aagatggcta tgtccagggt gaggagtaca tcgcggatct 720
gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780
ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tgggccactg 840
ggtgctgccc cctgcccagg accagcccct ggtggaagcc aaccacctgc tgcacgagag 900
cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggtaatt ggaacatgtt 960
tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgtg 1020
agcaccgcgc acctgccaca gcctcagagg cccgcacaat gaccggagga ggggccgctg 1080
tgggtctggc cctccctgt ccaggccccg caggaggcag atgcagtccc aggcctcctc 1140
ctgcccctgg gctctcaggg accccctggg tcggcttctg tccctgtcac accccaacc 1200
ccaggagggg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtctcc 1260
cagcccagac ccagggaccc ttggcccaa gctcagctct aagaaccgcc ccaaccctc 1320
cagctccaaa tctgagcctc caccacatag actgaaactc ccctggcccc agccctctcc 1380
tgccctggcct ggccctgggac acctcctctc tgccaggagg caataaaagc cagcgccggg 1440
accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaa 1503

```

<210> 221

<211> 328

<212> PRT

<213> Homo sapiens

<400> 221

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

1		5		10		15									
Gly	Ala	Gln	Gly	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln	Gly
		20						25					30		
Arg	Val	His	Gln	Ala	Ala	Pro	Leu	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala
		35					40					45			
His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	Gly	Arg	Glu	Val
	50					55					60				
Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser	Gln	Ala	Arg	Leu
65					70					75					80
Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Arg	Ala	Gly	Asp	Gly	Asp	Gly	Trp
				85					90					95	
Val	Ser	Leu	Ala	Glu	Leu	Arg	Ala	Trp	Ile	Ala	His	Thr	Gln	Gln	Arg
		100						105					110		
His	Ile	Arg	Asp	Ser	Val	Ser	Ala	Ala	Trp	Asp	Thr	Tyr	Asp	Thr	Asp
		115					120					125			
Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Glu	Leu	Arg	Asn	Ala	Thr	Tyr	Gly
	130					135					140				
His	Tyr	Ala	Pro	Gly	Glu	Glu	Phe	His	Asp	Val	Glu	Asp	Ala	Glu	Thr
145					150					155					160
Tyr	Lys	Lys	Met	Leu	Ala	Arg	Asp	Glu	Arg	Arg	Phe	Arg	Val	Ala	Asp
			165						170					175	
Gln	Asp	Gly	Asp	Ser	Met	Ala	Thr	Arg	Glu	Glu	Leu	Thr	Ala	Phe	Leu
		180						185					190		
His	Pro	Glu	Glu	Phe	Pro	His	Met	Arg	Asp	Ile	Val	Ile	Ala	Glu	Thr
		195					200					205			
Leu	Glu	Asp	Leu	Asp	Arg	Asn	Lys	Asp	Gly	Tyr	Val	Gln	Val	Glu	Glu
	210					215					220				
Tyr	Ile	Ala	Asp	Leu	Tyr	Ser	Ala	Glu	Pro	Gly	Glu	Glu	Glu	Pro	Ala
225				230						235					240
Trp	Val	Gln	Thr	Glu	Arg	Gln	Gln	Phe	Arg	Asp	Phe	Arg	Asp	Leu	Asn
			245					250						255	
Lys	Asp	Gly	His	Leu	Asp	Gly	Ser	Glu	Val	Gly	His	Trp	Val	Leu	Pro
		260					265						270		
Pro	Ala	Gln	Asp	Gln	Pro	Leu	Val	Glu	Ala	Asn	His	Leu	Leu	His	Glu
		275				280						285			

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcagggcct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe



<400> 225  
 cccccctgag cgacgctccc ccatgatgac gccacgga actt

44

<210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
 ggggccttgc cttccgcact cgggcgcagc cgggtggatc tgcagcaggt gggagcccc 60  
 gggcgggcgg cgcggtgctg agggatccct gacgcctctg tccctgtttc tttgtcgctc 120  
 ccagcctgtc tgcgtcgatt ttggcgcccc cgctccccg cgggtcgggg ttgcacaccg 180  
 atcctgggct tgcgtcgatt tgccgcagag gcgcctccca gacctagagg ggcgtggcc 240  
 tggagcagcg ggtcgctctgt gtcctctctc ctctgcgcg cgccgggga tccgaagggt 300  
 gcggggctct gaggaggtga cgcgcggggc ctccgcgacc ctggccttgc ccgcattctc 360  
 cctctctccc aggtgtgagc agcctatcag tcacctgtc cgagcctgg atcccggtc 420  
 tgggcctcgg tgtgtgtctg ctgctgtctc cggggcccg ggcagcagag ggagccgctc 480  
 ccattgctat cacatgtttt accagaggct tggacatcag gaaagagaaa gcagatgtcc 540  
 tctgccagag gggctgccct cttgaggaat tctctgtgta tgggaacata gtatatgctt 600  
 ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac tcagggggac 660  
 ctgtacgagt ctatagccta cctggctcag aaaactattc ctctagtagat gccaatggca 720  
 tccagtctca aatgctttct agatggtctg cttctttcac agtaactaaa ggcaaaagta 780  
 gtacacagga ggccacagga caagcagtggt ccacagcaca tccaccaaca ggtaaacgac 840  
 taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 900  
 tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag aattttgttg 960  
 gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1020  
 ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080  
 tgtttgccat aaaggaagta ggtttcagag ggggtaattc caatacagga aaagccttga 1140  
 agcatactgc tcagaaattc ttcacggtag atgctggagt aagaaaagg atcccaaaag 1200  
 tgggtggtgt atttattgat ggttggcctt ctgatgacat cgaggaagca ggcattgttg 1260  
 ccagagagtt tgggtgtcaat gtatttatag tttctgtggc caagcctatc cctgaagaac 1320  
 tggggatggt tcaggatgtc acattttgtt acaaggctgt ctgtcggaat aatggcttct 1380  
 tctcttacca catgcccac tggtttggca ccacaaaata cgtaaagcct ctggtacaga 1440  
 agctgtgcac tcatgaacaa atgatgtgca gcaagacctg ttataactca gtgaacattg 1500  
 cctttctaat tgatggctcc agcagtgttg gagatagcaa tttccgcctc atgcttgaat 1560  
 ttgtttccaa catagccaag acttttgaaa tctcggacat tgggtgccaag atagctgctg 1620  
 tacagtttac ttatgatcag cgcacggagt tcagtttcac tgactatagc accaaagaga 1680  
 atgtcctagc tgtcatcaga aacatccgct atatgagtgg tggacagct actggtgatg 1740  
 ccatttcctt cactgttaga aatgtgtttg gccctataag ggagagcccc aacaagaact 1800  
 tcctagtaat tgtcacagat gggcagtcct atgatgatgt ccaaggccct gcagctgctg 1860  
 cacatgatgc aggaatcact atcttctctg ttggtgtggc ttgggcacct ctggatgacc 1920  
 tgaaagatat ggcttctaaa ccgaaggagt ctacgccttt cttcacaaga gattcacag 1980  
 gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040  
 agcaataatg gtaacatttt gacaactgaa agaaaaagta caaggggatc cagtgtgtaa 2100  
 attgtattct cataactg aaatgcttta gcatactaga atcagatata aaactattaa 2160  
 gtatgtcaac agccatttag gcaaataagc actcctttta agccgctgcc ttctggttac 2220  
 aatttacagt gtactttgtt aaaaacactg ctgaggcttc ataactatgg ctcttagaaa 2280  
 ctcaggaaag aggagataat gtggattaaa accttaagag ttctaaccat gcctactaaa 2340  
 tgtacagata tgcaaattcc atagctcaat aaaagaatct gatacttaga ccaaaaaaaaa 2400  
 aaa 2403

<210> 227

<212> PRT

<400> 227

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe  
245 250 255



Phe Leu Glu Ser Gln Gln  
545 550

<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229

ctgctgtcca caggggag

18

<210> 230

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230

ccttgaagca tactgctc

18

<210> 231

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231

gagatagcaa tttccgcc

18

<210> 232

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232  
 ttcctcaaga gggcagcc 18

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233  
 cttggcacca atgtccgaga tttc 24

<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 234  
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235  
 <211> 2586  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
 cgccgcgctc ccgcacccgc ggcccgccca ccgcgcgcgt cccgcctctg caccgcgagc 60  
 ccggcgccct ccggcgggga gcgagcagat ccagtcgggc ccgcagcgca actcgggtcca 120  
 gtcggggcgcg cggctgcggg cgcagagcgg agatgcagcg gcttggggcc accctgctgt 180  
 gcttgcctgt ggcgcgggcg gtccccacgg ccccgcgcc cgctccgacg gcgacctcgg 240  
 ctccagtc aa gcccggcccc gctctcagct accgcagga ggaggccacc ctcaatgaga 300  
 tgttcgcgga ggttgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360  
 aagagatgga ggcagaagaa gtgctgcta aagcatcatc agaagtgaac ctggcaaaact 420  
 tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaat aataccatcc 480  
 atgtgcaccg agaaattcac aagataacca acaaccagac tggacaaatg gtcttttcag 540  
 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcacatcag 600  
 acgaggactg tgggcccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660  
 catgccgggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720



Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
85 90 95

Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
325 330 335

Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
340 345 350

&lt;210&gt; 237

<211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 237  
 ggagctgcac cccttg 17  
  
 <210> 238  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 238  
 ggaggactgt gccacatga gagactcttc aaaccaagg caaaattgg 49  
  
 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 239  
 gcagagcgga gatgcagcgg ctg 24  
  
 <210> 240  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 240  
 ttggcagctt catggagg 18  
  
 <210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 241  
 cctgggcaaa aatgcaac 18



<210> 242  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
 ctccagctcc tggcgacact cctc

24

<210> 243  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
 ggctctcagc taccgcgag gagcgaggcc accctcaatg agatg

45

<210> 244  
 <211> 3679  
 <212> DNA  
 <213> Homo Sapien

<400> 244  
 aaggaggctg ggaggaaaga ggtaagaaag gttagagaac ctacctcaca 50  
 tctctctggg ctcagaagga ctctgaagat aacaataatt tcagcccatc 100  
 cactctcctt cctctccaaa cacacatgtg catgtacaca cacacataca 150  
 cacacataca ccttcctctc cttcactgaa gactcacagt cactcactct 200  
 gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcctggcc 250  
 attacctctg cagctccttt ggcttggtga gtcaaaaaac atgggagggg 300  
 ccaggcacgg tgactcacac ctgtaatccc agcatttttg gagaccgagg 350  
 tgagcagatc acttgaggtc aggagtccga gaccagcctg gccaacatgg 400  
 agaaaccccc atctctacta aaaatacaaa aattagccag gagtgggtggc 450  
 aggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500  
 gaatccagga ggcggaggat gcagtcagct gagtgcaccg ctgcactcca 550  
 gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600

ggggtagata ctgcttctct gcaacctcct taactctgca tctcttcttt 650  
 ccagggtgc ccctgatggg gcctggcaat gactgagcag gcccagcccc 700  
 agaggacaag gaagagaagg catattgagg agggcaagaa gtgacgcccc 750  
 gtgtagaatg actgccctgg gaggttggtt ccttgggccc tggcagggtt 800  
 gctgaccctt accctgcaaa acacaaagag caggactcca gactctcctt 850  
 gtgaatggtc ccctgccttg cagctccacc atgaggcttc tcgtggcccc 900  
 actcttgcta gcttgggtgg ctggtgccac tgccactgtg cccgtggtac 950  
 cctggcatgt tccctgcccc cctcagtgtg cctgccagat ccggccctgg 1000  
 tatacgcccc gctcgtccta ccgcgaggct accactgtgg actgcaatga 1050  
 cctatttctg acggcagtc ccccggcact ccccgagggc acacagaccc 1100  
 tgctcctgca gagcaacagc attgtccgtg tggaccagag tgagctgggc 1150  
 tacctggcca atctcacaga gctggacctg tcccagaaca gcttttcgga 1200  
 tgcccagagac tgtgatttcc atgccctgcc ccagctgctg agcctgcacc 1250  
 tagaggagaa ccagctgacc cggctggagg accacagctt tgcagggtg 1300  
 gccagcctac aggaactcta tctcaaccac aaccagctct accgcatcgc 1350  
 cccaggggc ttttctggcc tcagcaactt gctgcggctg cacctcaact 1400  
 ccaacctcct gaggggcatt gacagccgtt ggtttgaaat gctgccaac 1450  
 ttggagatac tcatgattgg cggcaacaag gtagatgcca tcttgacat 1500  
 gaacttccgg cccctggcca acctgcgtag cctggtgcta gcaggcatga 1550  
 acctgcggga gatctccgac tatgccctgg aggggctgca aagcctggag 1600  
 agcctctcct tctatgacaa ccagctggcc cgggtgcca ggcgggcact 1650  
 ggaacaggtg cccgggctca agttcctaga cctcaacaag aaccgctcc 1700  
 agcgggtagg gccgggggac tttgccaaca tgctgcacct taaggagctg 1750  
 ggactgaaca acatggagga gctggtctcc atcgacaagt ttgccctgg 1800  
 gaacctcccc gagctgacca agctggacat caccaataac ccacggctgt 1850  
 ccttcatcca ccccgcgcc ttccaccacc tgcccagat ggagaccctc 1900  
 atgctcaaca acaacgctct cagtgccttg caccagcaga cggtgagtc 1950

cctgccaac	ctgcaggagg	taggtctcca	cggaacccc	atccgctgtg	2000
actgtgtcat	ccgctgggcc	aatgccacgg	gcacccgtgt	ccgcttcac	2050
gagccgcaat	ccaccctgtg	tgcggagcct	ccggacctcc	agcgctccc	2100
ggtccgtgag	gtgcccttcc	gggagatgac	ggaccactgt	ttgcccctca	2150
tctccccacg	aagcttcccc	ccaagcctcc	aggtagccag	tggagagagc	2200
atggtgctgc	attgccgggc	actggccgaa	cccgaacccg	agatctactg	2250
ggtcactcca	gctgggcttc	gactgacacc	tgcccatgca	ggcaggaggt	2300
accgggtgta	ccccgagggg	accctggagc	tgcggagggg	gacagcagaa	2350
gaggcagggc	tatacacctg	tgtggcccag	aacctggtgg	gggctgacac	2400
taagacggtt	agtgtggttg	tgggccgtgc	tctcctccag	ccaggcaggg	2450
acgaaggaca	ggggctggag	ctccgggtgc	aggagacca	cccctatcac	2500
atcctgctat	cttgggtcac	cccacccaac	acagtgtcca	ccaacctcac	2550
ctggtccagt	gcctcctccc	tccggggcca	ggggggccaca	gctctggccc	2600
gcctgcctcg	gggaaccac	agctacaaca	ttaccgcct	ccttcaggcc	2650
acggagtact	gggcctgcct	gcaagtggcc	tttgtgatg	cccacacca	2700
gttggcttgt	gtatgggcca	ggaccaaaga	ggccacttct	tgccacagag	2750
ccttagggga	tcgtcctggg	ctcattgcca	tcctggctct	cgctgtcctt	2800
ctcctggcag	ctgggctagc	ggcccacctt	ggcacaggcc	aaccagga	2850
gggtgtgggt	gggaggcggc	ctctccctcc	agcctgggct	ttctggggct	2900
ggagtcccc	ttctgtccgg	gttgtgtctg	ctccctcgt	cctgccctgg	2950
aatccaggga	ggaagctgcc	cagatcctca	gaaggggaga	cactgttgcc	3000
accattgtct	caaaattctt	gaagctcagc	ctgttctcag	cagtagagaa	3050
atcactagga	ctacttttta	ccaaaagaga	agcagtctgg	gccagatgcc	3100
ctgccaggaa	agggacatgg	accacgtgc	ttgaggcctg	gcagctgggc	3150
caagacagat	ggggctttgt	ggccctgggg	gtgcttctgc	agccttgaaa	3200
aagttgccct	tacctcctag	ggtcacctct	gctgccattc	tgaggaacat	3250

ctccaaggaa caggagggac tttggctaga gcctcctgcc tccccatctt 3300  
 ctctctgccc agaggtcctt gggcctggct tggtgtgcc ctacctgtgt 3350  
 ccccgggctg cacccttcc tttctcttt ctctgtacag tctcagttgc 3400  
 ttgtctttgt gcctcctggg caagggctga aggaggccac tccatctcac 3450  
 ctcggggggc tgccctcaat gtgggagtga cccagccag atctgaagga 3500  
 catttgggag agggatgcc aggaacgcct catctcagca gcctgggctc 3550  
 ggcattccga agctgacttt ctataggcaa tttgtacct ttgtggagaa 3600  
 atgtgtcacc tcccccaacc cgattcactc ttttctcctg ttttgtaaaa 3650  
 aataaaaata aataataaca ataaaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met	Arg	Leu	Leu	Val	Ala	Pro	Leu	Leu	Leu	Ala	Trp	Val	Ala	Gly	1	5	10	15
Ala	Thr	Ala	Thr	Val	Pro	Val	Val	Pro	Trp	His	Val	Pro	Cys	Pro	20	25	30	
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser	35	40	45	
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu	50	55	60	
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu	65	70	75	
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly	80	85	90	
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe	95	100	105	
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu	110	115	120	
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His	125	130	135	
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His	140	145	150	

Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser	155	160	165
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile	170	175	180
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	185	190	195
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	200	205	210
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	215	220	225
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	230	235	240
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	245	250	255
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	260	265	270
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	275	280	285
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser	290	295	300
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	305	310	315
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala	320	325	330
Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	335	340	345
Ala	Leu	Ser	Ala	Leu	His	Gln	Gln	Thr	Val	Glu	Ser	Leu	Pro	Asn	350	355	360
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	365	370	375
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	380	385	390
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	395	400	405
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys			

09030315-071001

				410					415					420
Leu	Pro	Leu	Ile	Ser 425	Pro	Arg	Ser	Phe	Pro 430	Pro	Ser	Leu	Gln	Val 435
Ala	Ser	Gly	Glu	Ser 440	Met	Val	Leu	His	Cys 445	Arg	Ala	Leu	Ala	Glu 450
Pro	Glu	Pro	Glu	Ile 455	Tyr	Trp	Val	Thr	Pro 460	Ala	Gly	Leu	Arg	Leu 465
Thr	Pro	Ala	His	Ala 470	Gly	Arg	Arg	Tyr	Arg 475	Val	Tyr	Pro	Glu	Gly 480
Thr	Leu	Glu	Leu	Arg 485	Arg	Val	Thr	Ala	Glu 490	Glu	Ala	Gly	Leu	Tyr 495
Thr	Cys	Val	Ala	Gln 500	Asn	Leu	Val	Gly	Ala 505	Asp	Thr	Lys	Thr	Val 510
Ser	Val	Val	Val	Gly 515	Arg	Ala	Leu	Leu	Gln 520	Pro	Gly	Arg	Asp	Glu 525
Gly	Gln	Gly	Leu	Glu 530	Leu	Arg	Val	Gln	Glu 535	Thr	His	Pro	Tyr	His 540
Ile	Leu	Leu	Ser	Trp 545	Val	Thr	Pro	Pro	Asn 550	Thr	Val	Ser	Thr	Asn 555
Leu	Thr	Trp	Ser	Ser 560	Ala	Ser	Ser	Leu	Arg 565	Gly	Gln	Gly	Ala	Thr 570
Ala	Leu	Ala	Arg	Leu 575	Pro	Arg	Gly	Thr	His 580	Ser	Tyr	Asn	Ile	Thr 585
Arg	Leu	Leu	Gln	Ala 590	Thr	Glu	Tyr	Trp	Ala 595	Cys	Leu	Gln	Val	Ala 600
Phe	Ala	Asp	Ala	His 605	Thr	Gln	Leu	Ala	Cys 610	Val	Trp	Ala	Arg	Thr 615
Lys	Glu	Ala	Thr	Ser 620	Cys	His	Arg	Ala	Leu 625	Gly	Asp	Arg	Pro	Gly 630
Leu	Ile	Ala	Ile	Leu 635	Ala	Leu	Ala	Val	Leu 640	Leu	Leu	Ala	Ala	Gly 645
Leu	Ala	Ala	His	Leu 650	Gly	Thr	Gly	Gln	Pro 655	Arg	Lys	Gly	Val	Gly 660
Gly	Arg	Arg	Pro	Leu 665	Pro	Pro	Ala	Trp	Ala 670	Phe	Trp	Gly	Trp	Ser 675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
                     680                    685                    690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
                     695                    700                    705

Leu Pro Pro Leu Ser Gln Asn Ser  
                     710

<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgccatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgctcg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

gcaagccaag gcgctgtttg agaagggtgaa gaagttccgg acccatgtgg 50

aggaggggga cattgtgtac cgcctctaca tgcggcagac catcatcaag 100

gtgatcaagt tcctctcat catctgtac accgtctact acgtgcacaa 150

catcaagtgc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200  
 accgcaccta ccgctgtgcc caccctctgg ccacactctt caagatcctg 250  
 gcgtccttct acatcagcct agtcactctt tacggcctca tctgcatgta 300  
 cacactgtgg tggatgctac ggcgctccct caagaagtac tcgtttgagt 350  
 cgatccgtga ggagagcagc tacagcgaca tccccgacgt caagaacgac 400  
 ttgccttca tgctgcacct cattgaccaa tacgaccgc tctactccaa 450  
 gcgcttcgcc gtcttcctgt cggaggtgag tgagaacaag ctgcggcagc 500  
 tgaacctcaa caacgagtgg acgctggaca agctccggca gcggctcacc 550  
 aagaacgcgc aggacaagct ggagctgcac ctgttcatgc tcagtggcat 600  
 ccctgacact gtgtttgacc tgggtggagct ggaggtcctc aagctggagc 650  
 tgatccccga cgtgaccatc ccgcccagca ttgcccagct cacgggcctc 700  
 aaggagctgt ggctctacca cacagcggcc aagattgaag cgcctgcgct 750  
 ggcttctctg cgcgagaacc tgcgggcgct gcacatcaag ttcaccgaca 800  
 tcaaggagat cccgctgtgg atctatagcc tgaagacact ggaggagctg 850  
 cacctgacgg gcaacctgag cgcgggagaac aaccgctaca tcgtcatcga 900  
 cgggctgcgg gagctcaaac gcctcaaggt gctgcggctc aagagcaacc 950  
 taagcaagct gccacagggtg gtcacagatg tgggcgtgca cctgcagaag 1000  
 ctgtccatca acaatgaggg caccaagctc atcgtcctca acagcctcaa 1050  
 gaagatggcg aacctgactg agctggagct gatccgctgc gacctggagc 1100  
 gcatccccca ctccatcttc agcctccaca acctgcagga gattgacctc 1150  
 aaggacaaca acctcaagac catcgaggag atcatcagct tccagcacct 1200  
 gcaccgcctc acctgcctta agctgtggta caaccacatc gcctacatcc 1250  
 ccatccagat cggcaacctc accaacctgg agcgcctcta cctgaaccgc 1300  
 aacaagatcg agaagatccc caccagctc ttctactgcc gcaagctgcg 1350  
 ctacctggac ctgagccaca acaacctgac ctctctccct gccgacatcg 1400  
 gcctcctgca gaacctccag aacctagcca tcacggccaa ccggatcgag 1450





aacggtgctc cattcgcacc tccccctcctc gtgcctgccc tgccctctcca 2850  
 cgcacagtgt taaggagcca agaggagcca cttcgcccag actttgtttc 2900  
 cccacctcct gcggcatggg tgtgtccagt gccaccgctg gcctccgctg 2950  
 cttccatcag ccctgtcgcc acctggctcct tcatgaagag cagacactta 3000  
 gaggctggtc gggaatgggg aggtcgcccc tgggagggca ggcgttggtt 3050  
 ccaagccggt tcccgtccct ggcgcctgga gtgcacacag cccagtcggc 3100  
 acctgggtggc tggaagccaa cctgcttttag atcactcggg tccccacctt 3150  
 agaagggtcc ccgccttaga tcaatcacgt ggacactaag gcacgtttta 3200  
 gagtctcttg tcttaatgat tatgtccatc cgtctgtccg tccatttggtg 3250  
 ttttctgcgt cgtgtcattg gatataatcc tcagaaataa tgcacactag 3300  
 cctctgacaa ccatgaagca aaaatccgtt acatgtgggt ctgaacttgt 3350  
 agactcggtc acagtatcaa ataaaatcta taacagaaaa aaaaaaaaaa 3400

a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile
1				5					10				15	

Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
			20						25				30	

Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
			35						40				45	

Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
			50						55				60	

Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
			65						70				75	

Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
			80						85				90	

Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	95		100		105
Asn Asp Phe Ala	Phe Met Leu His Leu	Ile Asp Gln Tyr Asp	Pro		
	110		115		120
Leu Tyr Ser Lys	Arg Phe Ala Val Phe	Leu Ser Glu Val Ser	Glu		
	125		130		135
Asn Lys Leu Arg	Gln Leu Asn Leu Asn	Asn Glu Trp Thr Leu	Asp		
	140		145		150
Lys Leu Arg Gln	Arg Leu Thr Lys Asn	Ala Gln Asp Lys Leu	Glu		
	155		160		165
Leu His Leu Phe	Met Leu Ser Gly Ile	Pro Asp Thr Val Phe	Asp		
	170		175		180
Leu Val Glu Leu	Glu Val Leu Lys Leu	Glu Leu Ile Pro Asp	Val		
	185		190		195
Thr Ile Pro Pro	Ser Ile Ala Gln Leu	Thr Gly Leu Lys Glu	Leu		
	200		205		210
Trp Leu Tyr His	Thr Ala Ala Lys Ile	Glu Ala Pro Ala Leu	Ala		
	215		220		225
Phe Leu Arg Glu	Asn Leu Arg Ala Leu	His Ile Lys Phe Thr	Asp		
	230		235		240
Ile Lys Glu Ile	Pro Leu Trp Ile Tyr	Ser Leu Lys Thr Leu	Glu		
	245		250		255
Glu Leu His Leu	Thr Gly Asn Leu Ser	Ala Glu Asn Asn Arg	Tyr		
	260		265		270
Ile Val Ile Asp	Gly Leu Arg Glu Leu	Lys Arg Leu Lys Val	Leu		
	275		280		285
Arg Leu Lys Ser	Asn Leu Ser Lys Leu	Pro Gln Val Val Thr	Asp		
	290		295		300
Val Gly Val His	Leu Gln Lys Leu Ser	Ile Asn Asn Glu Gly	Thr		
	305		310		315
Lys Leu Ile Val	Leu Asn Ser Leu Lys	Lys Met Ala Asn Leu	Thr		
	320		325		330
Glu Leu Glu Leu	Ile Arg Cys Asp Leu	Glu Arg Ile Pro His	Ser		
	335		340		345
Ile Phe Ser Leu	His Asn Leu Gln Glu	Ile Asp Leu Lys Asp	Asn		
	350		355		360

09903645-071004

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His  
 365 370 375  
 Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile  
 380 385 390  
 Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu  
 395 400 405  
 Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys  
 410 415 420  
 Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe  
 425 430 435  
 Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala  
 440 445 450  
 Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln  
 455 460 465  
 Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln  
 470 475 480  
 Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile  
 485 490 495  
 Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly  
 500 505 510  
 Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp  
 515 520 525  
 Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg  
 530 535 540  
 Ala Asp Lys Glu Gln Ala  
 545

<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

caacaatgag ggcaccaagc 20

<210> 252

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

gcctgttget gatgctgccg tgcggtactt gtcattggagc tggcactgcg 50  
 gcgctctccc gtcccgcggt ggttgetget getgccgetg ctgctgggccc 100  
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
 tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtgggtcta 200  
 ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250  
 ggcttcaggg cggccagggc ggttctagca ctggatttgg aaactttgag 300  
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350  
 ccaggctgcc agtctcctat ttgtggataa tcccgtagggc actgggttca 400  
 gttatgtgaa tggtagtggc gcctatgcca aggacctggc tatggtggct 450  
 tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500  
 ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550  
 cagctggcat tggcttagag ctttataagg ccattcagcg agggaccatc 600  
 aagtgcact ttgcgggggt tgccttgggt gattcctgga tctcccctgt 650  
 tgattcgggt ctctcctggg gaccttacct gtacagcatg tctcttctcg 700

aagacaaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750  
gccgtaaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800  
agaaatgatc attgaacaga acacagatgg ggtgaacttc tataacatct 850  
taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900  
cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950  
agatgcctta agccagctca tgaatggccc catcagaaag aagctcaaaa 1000  
ttattcctga ggatcaatcc tggggaggcc aggtaccaa cgtctttgtg 1050  
aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100  
gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150  
tcgtagatac catgggtcag gaggcctggg tgcggaaact gaagtggcca 1200  
gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250  
taaactcttg gaaacatctg cttttgtcaa gtcctacaag aaccttgctt 1300  
tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350  
atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400  
gggctggaga tgagctggtt tggccttggg gcacagagct gagctgaggc 1450  
cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500  
gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550  
ggaggcaatt tggaaattat ttctgcttct taaaaaaacc taagattttt 1600  
taaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
1				5					10				15	
Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
			20					25					30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
			35					40					45	

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	
				50					55					60	
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	
				65					70					75	
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	
				80					85					90	
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	
				95					100					105	
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	
				110					115					120	
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu	
				125					130					135	
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	
				140					145					150	
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	
				155					160					165	
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	
				170					175					180	
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	
				185					190					195	
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	
				200					205					210	
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	
				215					220					225	
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	
				230					235					240	
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	
				245					250					255	
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	
				260					265					270	
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	
				275					280					285	
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	
				290					295					300	
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly	

	305		310		315
Pro Ile Arg Lys	Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp			
	320	325			330
Gly Gly Gln Ala	Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe			
	335	340			345
Met Lys Pro Val	Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly			
	350	355			360
Ile Asn Val Thr	Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp			
	365	370			375
Thr Met Gly Gln	Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu			
	380	385			390
Leu Pro Lys Phe	Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp			
	395	400			405
Pro Lys Ser Leu	Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn			
	410	415			420
Leu Ala Phe Tyr	Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser			
	425	430			435
Asp Gln Gly Asp	Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln			
	440	445			450
Gln Glu					

&lt;210&gt; 256

&lt;211&gt; 1100

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 256

ggccgcggga gaggaggcca tgggcgcgcg cggggcgctg ctgctggcgc 50

tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100

ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150

tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgcgcc tgctcagcca ccgctgggca 250

ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300

cgggtggatg gtccagtttg gccagctgac ttccatgccca tccttctgga 350

gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400



cctcgctacc tggggaattc accctatgac attgccttgg tgaagctgtc 450  
 tgcacctgtc acctacacta aacacatcca gcccatctgt ctccaggcct 500  
 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550  
 tacatcaaag aggatgaggc actgccatct cccacacccc tccaggaagt 600  
 tcaggtcgcc atcataaaca actctatgtg caaccacctc ttcctcaagt 650  
 acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700  
 caaggcggga aggatgcctg cttcggtgac tcaggtggac ccttggcctg 750  
 taacaagaat ggactgtggt atcagattgg agtcgtgagc tggggagtgg 800  
 gctgtggtcg gcccaatcgg ccggtgtct acaccaatat cagccaccac 850  
 tttgagtga tccagaagct gatggcccag agtggcatgt ccagccaga 900  
 cccctcctgg ccactactct tttccctct tctctgggt ctccactcc 950  
 tggggccggt ctgagcctac ctgagcccat gcagcctggg gccactgcc 1000  
 agtcaggccc tggttctctt ctgtcttgtt tggtaataaa cacattccag 1050  
 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ala	Arg
1				5					10					15

Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
				20					25				30	

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
			35						40				45	

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
			50						55				60	

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
			65						70				75	

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
			80						85				90	

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
 95 100 105  
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
 110 115 120  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
 125 130 135  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
 140 145 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
 155 160 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
 170 175 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
 185 190 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
 200 205 210  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
 215 220 225  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
 230 235 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
 245 250 255  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
 260 265 270  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
 275 280 285  
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu  
 290 295 300  
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val  
 305 310

&lt;210&gt; 258

&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

cccacgcgtc cgcggacgcg tgggaagggc agaatgggac tccaagcctg 50

cctcctaggg ctctttgccc tcatcctctc tggcaaatgc agttacagcc 100  
 cggagcccga ccagcggagg acgtgcccc caggctgggt gtccctgggc 150  
 cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200  
 gaatgtggaa agactctcgg agctgggtgca ggctgtgtcg gatcccagct 250  
 ctctcaata cggaaaatac ctgaccctag agaatgtggc tgatctgggtg 300  
 aggccatccc cactgaccct ccacacgggtg caaaaatggc tcttggcagc 350  
 cggagcccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400  
 ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagtttcat 450  
 cactatgtgg gaggacctac ggaaacccat gttgtaaggc cccacatcc 500  
 ctaccagctt ccacaggcct tggccccca tgtggacttt gtggggggac 550  
 tgcaccgttt tcccccaaca tcatccctga ggcaacgtcc tgagccgcag 600  
 gtgacagga ctgtaggcct gcatctgggg gtaacccct ctgtgatccg 650  
 taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700  
 acagccaagc ctgtgcccag ttctgggagc agtatttcca tgactcagac 750  
 ctggctcagt tcatgcgcct ctccgggtggc aactttgcac atcaggcatc 800  
 agtagcccg gtggttgagc aacagggccg gggccgggccc gggattgagg 850  
 ccagtctaga tgtgcagtac ctgatgagt ctggtgccaa catctccacc 900  
 tgggtctaca gtagccctgg ccggcatgag ggacaggagc ccttctgca 950  
 gtggctcatg ctgctcagta atgagtcagc cctgccacat gtgcatactg 1000  
 tgagctatgg agatgatgag gactccctca gcagcgccta catccagcgg 1050  
 gtcaacactg agctcatgaa ggctgccgct cgggggtctca cctgctctt 1100  
 cgctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150  
 agttccgccc taccttcctt gcctccagcc cctatgtcac cacagtggga 1200  
 ggcacatcct tccaggaacc tttcctcatc aaaaatgaaa ttgttgacta 1250  
 tatcagtggg ggtgggttca gcaatgtgtt cccacggcct tcataccagg 1300  
 aggaagctgt aacgaagttc ctgagctcta gccccacct gccaccatcc 1350  
 agttacttca atgccagtgg ccgtgcctac ccagatgtgg ctgcactttc 1400

tgatggctac tgggtgggtca gcaacagagt gccattcca tgggtgtccg 1450  
 gaacctcggc ctctactcca gtgtttgggg ggatcctatc cttgatcaat 1500  
 gagcacagga tccttagtgg cgcgcgcctt cttggctttc tcaacccaag 1550  
 gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600  
 atgagtcctg tctggatgaa gaggtagagg gccagggttt ctgctctggg 1650  
 cctggctggg atcctgtaac aggtggggga acaccaactt ccagctttg 1700  
 ctgaagactc tactcaaccc ctgacccttt cctatcagga gagatggctt 1750  
 gtccctgcc ctgaagctgg cagttcagtc ccttattctg ccctgttggg 1800  
 agccctgctg aacctcaac tattgactgc tgcagacagc ttatctccct 1850  
 aacctgaaa tgctgtgagc ttgacttgac tcccaacct accatgctcc 1900  
 atcatactca ggtctcccta ctctgcctt agattcctca ataagatgct 1950  
 gtaactagca ttttttgaat gcctctccct ccgcatctca tctttctctt 2000  
 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050  
 acttgatatt cattcccca ttactgcaa ggagacctct actgtcaccg 2100  
 tttactcttt cctaccctga catccagaaa caatggcctc cagtgcatac 2150  
 ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200  
 ccttacttag cttccaggtc ttaacttctc tgactactct tgtcttctc 2250  
 tctcatcaat ttctgcttct tcatggaatg ctgaccttca ttgctccatt 2300  
 tgtagatttt tgctcttctc agtttactca ttgtccctg gaacaaatca 2350  
 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400  
 aatgattgat acctcaaatg taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln	Ala	Cys	Leu	Leu	Gly	Leu	Phe	Ala	Leu	Ile	Leu
1				5				10					15	

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

				20					25					30
Leu	Pro	Pro	Gly	Trp 35	Val	Ser	Leu	Gly	Arg 40	Ala	Asp	Pro	Glu	Glu 45
Glu	Leu	Ser	Leu	Thr 50	Phe	Ala	Leu	Arg	Gln 55	Gln	Asn	Val	Glu	Arg 60
Leu	Ser	Glu	Leu	Val 65	Gln	Ala	Val	Ser	Asp 70	Pro	Ser	Ser	Pro	Gln 75
Tyr	Gly	Lys	Tyr	Leu 80	Thr	Leu	Glu	Asn	Val 85	Ala	Asp	Leu	Val	Arg 90
Pro	Ser	Pro	Leu	Thr 95	Leu	His	Thr	Val	Gln 100	Lys	Trp	Leu	Leu	Ala 105
Ala	Gly	Ala	Gln	Lys 110	Cys	His	Ser	Val	Ile 115	Thr	Gln	Asp	Phe	Leu 120
Thr	Cys	Trp	Leu	Ser 125	Ile	Arg	Gln	Ala	Glu 130	Leu	Leu	Leu	Pro	Gly 135
Ala	Glu	Phe	His	His 140	Tyr	Val	Gly	Gly	Pro 145	Thr	Glu	Thr	His	Val 150
Val	Arg	Ser	Pro	His 155	Pro	Tyr	Gln	Leu	Pro 160	Gln	Ala	Leu	Ala	Pro 165
His	Val	Asp	Phe	Val 170	Gly	Gly	Leu	His	Arg 175	Phe	Pro	Pro	Thr	Ser 180
Ser	Leu	Arg	Gln	Arg 185	Pro	Glu	Pro	Gln	Val 190	Thr	Gly	Thr	Val	Gly 195
Leu	His	Leu	Gly	Val 200	Thr	Pro	Ser	Val	Ile 205	Arg	Lys	Arg	Tyr	Asn 210
Leu	Thr	Ser	Gln	Asp 215	Val	Gly	Ser	Gly	Thr 220	Ser	Asn	Asn	Ser	Gln 225
Ala	Cys	Ala	Gln	Phe 230	Leu	Glu	Gln	Tyr	Phe 235	His	Asp	Ser	Asp	Leu 240
Ala	Gln	Phe	Met	Arg 245	Leu	Phe	Gly	Gly	Asn 250	Phe	Ala	His	Gln	Ala 255
Ser	Val	Ala	Arg	Val 260	Val	Gly	Gln	Gln	Gly 265	Arg	Gly	Arg	Ala	Gly 270
Ile	Glu	Ala	Ser	Leu 275	Asp	Val	Gln	Tyr	Leu 280	Met	Ser	Ala	Gly	Ala 285

Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly	290	295	300
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser	305	310	315
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp	320	325	330
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met	335	340	345
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp	350	355	360
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg	365	370	375
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly	380	385	390
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp	395	400	405
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser	410	415	420
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His	425	430	435
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro	440	445	450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg	455	460	465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val	470	475	480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser	485	490	495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln	500	505	510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser	515	520	525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro	530	535	540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu	545	550	555

09302615.071004

Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

```

gccgcgcgct ctctcccgcc gccacacact gtctgagcgg cgcagcgagc 50
cgcgccccgg gcgggctgct cggcgcgga cagtgtcgg catggcaggg 100
attccagggc tcctcttctt tctcttcttt ctgctctgtg ctgttgggca 150
agtgagccct tacagtgcc cctggaaacc cacttggcct gcataccgcc 200
tcctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300
taagggaaact ccaactgcca cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500
tcagcatttt tgggaaggac ttctgtctca actacccttt ctcaacatca 550
gtgaagtat ccacgggctg caccggcacc ctggtggcag agaagcatgt 600
cctcacagct gccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgggc ttcttaaagc ccaagtttaa agatggtggt 700
cgaggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800
atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctctgtctaa 900
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgtcttacc agcaatgcga tgcccagcca ggggccagcg ggtctgggg 1050
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100

```

ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
 gatttcaacg tggctgtcag aatcactcct ctcaaatatg cccagatttg 1200  
 ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250  
 ttccctcctg gcagcaatta agggctcttca tgttcttatt ttaggagagg 1300  
 ccaaattggt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
 tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400  
 tgactggctt tactatttga aaactgggtt gtgtatcata tcatatatca 1450  
 ttttaagcagt ttgaaggcat acttttgcac agaaataaaa aaaataactga 1500  
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550  
 caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600  
 atatttggca tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu	1	5	10	15
Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro	20	25	30	
Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr	35	40	45	
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu	50	55	60	
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu	65	70	75	
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu	80	85	90	
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile	95	100	105	
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser	110	115	120	



Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser  
 125 130 135  
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe  
 140 145 150  
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val  
 155 160 165  
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly  
 170 175 180  
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu  
 185 190 195  
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr  
 200 205 210  
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys  
 215 220 225  
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp  
 230 235 240  
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro  
 245 250 255  
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys  
 260 265 270  
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp  
 275 280 285  
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu  
 290 295 300  
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala  
 305 310 315  
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln  
 320 325 330  
 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp  
 335 340 345  
 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg  
 350 355 360  
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly  
 365 370 375  
 Asn Tyr Leu Asp Cys Arg Glu Gly  
 380

<210> 262  
 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

<400> 262  
 gcatcgccct gggctctctcg agcctgctgc ctgctcccc gccccaccag 50  
 ccatgggtggg ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100  
 accttcacct ccctgctgct gctggcgctg acagccatcc tcaatgcggc 150  
 caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200  
 ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
 atccagaaga atgggaccca ccactgcgca gggtctctgc tcaccagccg 300  
 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350  
 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
 cgggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450  
 ctggaaggaa ggtgcctgtg cagacattgc cctgggtgct ctcgagcgct 500  
 ccatacagtt ctcagagcgg gtccctgcca tctgcctacc tgatgcctct 550  
 atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600  
 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650  
 ttctatcat cgactcgga gtctgcagcc atctgtactg gcggggagca 700  
 ggacagggac ccatactga ggacatgctg tgtgccggt acttgagggg 750  
 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggtgt 850  
 gccgagcgca acaggcccgg ggtctacatc agcctctctg cgcaccgctc 900  
 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950  
 ggggtggggc cctcagggca ccgagccagg gctctggggc cgcgcgcgc 1000  
 tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
 cacatctgga tctggatctg cggcggcctc gggcggtttc ccccgccgta 1100  
 aataggctca tctacctta cctctggggg cccggacggc tgctgcggaa 1150

aggaaacccc ctccccgacc cgccccgacgg cctcaggccc ccctccaagg 1200  
 catcaggccc cgccccacgg cctcatgtcc ccgccccac gacttccggc 1250  
 cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300  
 ataggatatt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350  
 ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

Arg Ser

<211> 24

<213> Artificial Sequence

### <223> Synthetic Oligonucleotide Probe

gtccgcaagg atgcctacat gttc 24

<211> 19

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

gcagaggtgt ctaaggttg 19

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 266  
agctctagac caatgccagc ttcc 24

<210> 267  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 267  
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 268  
ggggaattca ccctatgaca ttgcc 25

<210> 269  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 269  
gaatgccctg caagcatcaa ctgg 24

<210> 270  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 270  
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatgggac tccaag 26

<210> 272  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 274  
ggcgaagagc agggtgagac cccg 24

<210> 275  
<211> 45

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gccctcatcc tctctggcaa atgcagttac agcccggagc ccgac 45

<210> 276  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
gggcagggat tccagggctc c 21

<210> 277  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcaggttc 18

<210> 278  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcatcgatt gctggtagag caag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataaccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gtcataaca gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctgggcg actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaagggtcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100



agatgaggag aaacgtttga tggaggagct gcacaacctc taccgggccc 150  
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt gggggccaaa 250  
 caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300  
 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350  
 tacaacctca gcgcgccac ctgcagccca ggccagatgt gcggccacta 400  
 cacgcagggtg gtatgggcca agacagagag gatcggctgt ggttcccact 450  
 tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500  
 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550  
 ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600  
 tctgtgaacc catcggaagc ccggaagatg ctccaggattt gccttacctg 650  
 gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700  
 aatgggtact ccttcttccc tagcaacggg gattccggct ttcttggtaa 750  
 cagagggtctc aggtcctctg gcaaccaagg ctctgcctgc tgtggaaacc 800  
 caggccccaa cttccttagc aacgaaagac ccgcccctca tggcaacaga 850  
 ggctccacct tgcgtaacaa ctgagggtccc ttccattttg gcagctcaca 900  
 gcctgccctc cttggatgag gagccagtta ccttcccaa atcgacccat 950  
 gttcctatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000  
 ctctaggagc ccagagaact ctctggacct caagatgtcc ctgacagggg 1050  
 caagggaact cctaccccat gccaggagg aggtgaggc tgaggctgag 1100  
 ttgcctcctt ccagtgaggt cttggcctca gtttttccag ccaggacaa 1150  
 gccagggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200  
 agtccttgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250  
 gggcgtgcc tggtctgca gtcgtccttg ccagggtgag agggccctga 1300  
 caagcctagc gttgtgtcag ggctgaactc gggccctggg catgtgtggg 1350  
 gccctctcct gggactactg ctctgcctc ctctggtgtt ggctggaatc 1400

ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450  
 catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500  
 ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550  
 atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600  
 ggactgcaca ccggggccac acctctcctg cccctccctc ctgagtcctg 1650  
 ggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700  
 tgccacacaca gcatgtgctc tctccctgag tgctgtgta gctggggatg 1750  
 gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800  
 tgagtggggg aggcagggac gagggaagga aagtaactcc tgactctcca 1850  
 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu					
1				5					10					15					
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp					
				20					25					30					
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala					
				35					40					45					
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp					
				50					55					60					
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val					
				65					70					75					
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe					
				80					85					90					
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu					
				95					100					105					
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys					
				110					115					120					
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala					
				125					130					135					

Lys Thr Glu Arg	Ile Gly Cys Gly Ser	His Phe Cys Glu Lys	Leu
	140	145	150
Gln Gly Val Glu	Glu Thr Asn Ile Glu	Leu Leu Val Cys Asn	Tyr
	155	160	165
Glu Pro Pro Gly	Asn Val Lys Gly Lys	Arg Pro Tyr Gln Glu	Gly
	170	175	180
Thr Pro Cys Ser	Gln Cys Pro Ser Gly	Tyr His Cys Lys Asn	Ser
	185	190	195
Leu Cys Glu Pro	Ile Gly Ser Pro Glu	Asp Ala Gln Asp Leu	Pro
	200	205	210
Tyr Leu Val Thr	Glu Ala Pro Ser Phe	Arg Ala Thr Glu Ala	Ser
	215	220	225
Asp Ser Arg Lys	Met Gly Thr Pro Ser	Ser Leu Ala Thr Gly	Ile
	230	235	240
Pro Ala Phe Leu	Val Thr Glu Val Ser	Gly Ser Leu Ala Thr	Lys
	245	250	255
Ala Leu Pro Ala	Val Glu Thr Gln Ala	Pro Thr Ser Leu Ala	Thr
	260	265	270
Lys Asp Pro Pro	Ser Met Ala Thr Glu	Ala Pro Pro Cys Val	Thr
	275	280	285
Thr Glu Val Pro	Ser Ile Leu Ala Ala	His Ser Leu Pro Ser	Leu
	290	295	300
Asp Glu Glu Pro	Val Thr Phe Pro Lys	Ser Thr His Val Pro	Ile
	305	310	315
Pro Lys Ser Ala	Asp Lys Val Thr Asp	Lys Thr Lys Val Pro	Ser
	320	325	330
Arg Ser Pro Glu	Asn Ser Leu Asp Pro	Lys Met Ser Leu Thr	Gly
	335	340	345
Ala Arg Glu Leu	Leu Pro His Ala Gln	Glu Glu Ala Glu Ala	Glu
	350	355	360
Ala Glu Leu Pro	Pro Ser Ser Glu Val	Leu Ala Ser Val Phe	Pro
	365	370	375
Ala Gln Asp Lys	Pro Gly Glu Leu Gln	Ala Thr Leu Asp His	Thr
	380	385	390
Gly His Thr Ser	Ser Lys Ser Leu Pro	Asn Phe Pro Asn Thr	Ser
	395	400	405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
 455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

gtaactgaag tcaggctttt catttgggaa gccccctcaa cagaattcgg 50

tcattctcca agttatggtg gacgtacttc tgttgttctc cctctgcttg 100  
 ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150  
 caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200  
 acaacaatga attggagacc attccaaatc tgggaccagt ctcggaat 250  
 attacacttc tctccttggc tggaaacagg attggtgaaa tactccctga 300  
 acatctgaaa gagtttcagt ccttgaaac tttggacctt agcagcaaca 350  
 atatttcaga gtcctaaact gcatttccag cctacagct caaatatctg 400  
 tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgaaa 450  
 tttggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500  
 ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550  
 aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttgg 600  
 tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650  
 atggagcttt ttgggggctg agcaacatgg aaattttgca gctggaccat 700  
 aacaacctaa cagagattac caaaggctgg ctttacgget tgetgatgct 750  
 gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800  
 cctgggagtt ctgccagaag ctcaagtgcg tggacctaac tttcaatcac 850  
 ttatcaaggt tagatgattc aagcttcctt ggccctaagct tactaaatac 900  
 actgcacatt gggaaacaaca gagtcagcta cattgctgat tgtgccttcc 950  
 gggggctttc cagtttaaag actttggatc tgaagaacaa tgaaatttcc 1000  
 tggactattg aagacatgaa tgggtgctttc tctgggcttg acaaactgag 1050  
 gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100  
 tcaactggtt ggatgcattg gagcatctag acctgagtga caacgcaatc 1150  
 atgtctttac aaggcaatgc attttcacaa atgaagaaac tgcaacaatt 1200  
 gcattttaat acatcaagcc ttttgtgcga ttgccagcta aaatggctcc 1250  
 cacagtgggt ggcggaacaa aactttcaga gctttgtaaa tgccagttgt 1300  
 gcccatcctc agctgctaaa aggaagaagc atttttgctg ttagccaga 1350

tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400  
 aaacacagtc ggcaataaaa ggttccaatt tgagtttcat ctgctcagct 1450  
 gccagcagca gtgattcccc aatgactttt gcttggaana aagacaatga 1500  
 actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggccaag 1550  
 gtggcgaggt gatggagtat accaccatcc ttccgctgcg cgaggtggaa 1600  
 tttgccagtg aggggaaata tcagtgtgtc atctccaatc actttgggtc 1650  
 atcctactct gtcaaagcca agcttacagt aaatatgctt cctcattca 1700  
 ccaagacccc catggatctc accatccgag ctggggccat ggcacgcttg 1750  
 gagtgtgctg ctgtggggca ccagccccc cagatagcct ggcagaagga 1800  
 tgggggcaca gacttcccag ctgcacggga gagacgcatg catgtgatgc 1850  
 ccgaggatga cgtgttcttt atcgtggatg tgaagataga ggacattggg 1900  
 gtatacagct gcacagctca gaacagtgcg ggaagtattt cagcaaatgc 1950  
 aactctgact gtcctagaaa caccatcatt tttcgggcca ctgttgacc 2000  
 gaactgtaac caaggagaa acagccgtcc tacagtgcac tgctggagga 2050  
 agccctcccc cttaaactgaa ctggacaaa gatgatagcc cattggtggt 2100  
 aaccgagagg cacttttttg cagcaggcaa tcagcttctg attattgtgg 2150  
 actcagatgt cagtgatgct gggaaatata catgtgagat gtctaacacc 2200  
 cttggcactg agagaggaaa cgtgcgcctc agtgtgatcc ccaactcaac 2250  
 ctgcgactcc cctcagatga cagccccatc gttagacgat gacggatggg 2300  
 ccaactgtggg tgtcgtgatc atagccgtgg tttgctgtgt ggtgggcacg 2350  
 tcactcgtgt ggggtggtcat catataccac acaaggcggg ggaatgaaga 2400  
 ttgcagcatt accaacacag atgagaccaa cttgccagca gatattccta 2450  
 gttatttgtc atctcagggg acgttagctg acaggcagga tgggtacgtg 2500  
 tcttcagaaa gtggaagcca ccaccagttt gtcacatctt caggtgctgg 2550  
 atttttctta ccacaacatg acagtagtgg gacctgcat attgacaata 2600  
 gcagtgaagc tgatgtggaa gctgccacag atctgttcct ttgtccgttt 2650  
 ttgggatcca caggccctat gtatttgaag ggaaatgtgt atggctcaga 2700

tccttttgaa acatatcata caggttgcag tcctgaccca agaacagttt 2750  
 taatggacca ctatgagccc agttacataa agaaaaagga gtgctaccca 2800  
 tgttctcatc cttcagaaga atcctgcgaa cggagcttca gtaatatac 2850  
 gtggccttca catgtgagga agctacttaa cactagttac tctcacaatg 2900  
 aaggacctgg aatgaaaaat ctgtgtctaa acaagtcctc tttagatttt 2950  
 agtgcaaatc cagagccagc gtcggttgcc tcgagtaatt ctttcatggg 3000  
 tacctttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050  
 ttggacagcc atcagattgt cagccaagag ccttttattt gaaagctcat 3100  
 tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150  
 agattttcag gaagaaaatc acatttgtac ctttaaacag actttagaaa 3200  
 actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250  
 tgagaccaa ggaaaagctt aacatactac ctcaagtga cttttattta 3300  
 aaagagagag aatcttatgt tttttaaatg gagttatgaa ttttaaaagg 3350  
 ataaaaatgc tttatttata cagatgaacc aaaattacaa aaagttatga 3400  
 aaatttttat actgggaatg atgctcatat aagaatacct ttttaaacta 3450  
 tttttaact ttgttttatg caaaaaagta tcttacgtaa attaatagata 3500  
 taaatcatga ttattttatg tatttttata atgccagatt tctttttatg 3550  
 gaaaatgagt tactaaagca ttttaaataa tacctgcctt gtaccatttt 3600  
 ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650  
 tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met	Val	Asp	Val	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Leu	Leu	Phe	His
1				5					10				15	

Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20					25				30	

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	35	40	45
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	50	55	60
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	65	70	75
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	80	85	90
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	95	100	105
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	110	115	120
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	125	130	135
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	140	145	150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	155	160	165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	185	190	195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	230	235	240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	245	250	255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	260	265	270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser			

09902645-071004



	290		295		300
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile	305		310		315
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg	320		325		330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala	335		340		345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn	350		355		360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys	365		370		375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys	380		385		390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln	395		400		405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly	410		415		420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp	425		430		435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala	440		445		450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser	455		460		465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu	470		475		480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln	485		490		495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu	500		505		510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn	515		520		525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn	530		535		540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg	545		550		555

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
560	565		570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
575	580		585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
590	595		600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
605	610		615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
620	625		630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635	640		645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650	655		660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
665	670		675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680	685		690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695	700		705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710	715		720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725	730		735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
740	745		750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755	760		765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770	775		780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
785	790		795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
800	805		810

<210> 291  
<211> 2906

<213> Homo Sapien

1000-1050

ggggagagga attgaccatg taaaaggaga cttttttttt tgggtggtggt 50

ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100

tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150

gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200

acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250

ttggtgtggt ctgacataaa taaataatct taaagcagct gttccctctc 300

ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacia 350

agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400

gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450

ggtgtggtgg tgttttcctt tctttttgaa tttcccacia gaggagagga 500

aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550

gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600

tttgtgcta tgttgactaa aattgacgga taattgcagt tggatttttc 650

ttcatcaacc tccttttttt taaattttta ttctttttgg tatcaagatc 700

atgcgttttc tcttgttctt aaccacctgg atttccatct ggatgttgct 750

gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800

ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850

ataggctcta gggttaacag ggccctattt gaccccttgc ttgtggtgct 900

gctggctctt caacttcttg tgggtggtgg tctggtgcgg gctcagacct 950

gcccttctgt gtgctcctgc agcaaccagt tcagcaagggt gatttgtggt 1000

cggaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050

gctgaacctc catgagaacc aaatccagat catcaaagtg aacagcttca 1100

agcattgag gcacttgga atcctacagt tgagtaggaa ccatatcaga 1150

accattgaaa ttggggcttt caatgggtctg gcgaacctca acactctgga 1200

actctttgac aatcgtctta ctaccatccc gaatggagct tttgtatact 1250

tgtctaaact gaaggagctc tggttgcgaa acaaccccat tgaaagcatc 1300  
 ctttcttatg cttttaacag aattccttct ttgcgccgac tagacttagg 1350  
 ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggtctgt 1400  
 ccaacttgag gtatttgaac cttgccatgt gcaaccttcg ggaaatccct 1450  
 aacctcacac cgctcataaa actagatgag ctggatcttt ctgggaatca 1500  
 tttatctgcc atcaggcctg gctctttcca gggtttgatg caccttcaaa 1550  
 aactgtggat gatacagtcc cagattcaag tgattgaacg gaatgccttt 1600  
 gacaaccttc agtcactagt ggagatcaac ctggcacaca ataactaac 1650  
 attactgcct catgacctct tactccctt gcatcatcta gagcggatac 1700  
 atttacatca caacccttgg aactgtaact gtgacatact gtggctcagc 1750  
 tggtgagataa aagacatggc cccctcgaac acagcttggt gtgcccggtg 1800  
 taacactcct cccaatctaa aggggaggtta cattggagag ctgcaccaga 1850  
 attacttcac atgctatgct ccggtgattg tggagcccc tgcagacctc 1900  
 aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950  
 cctgacatct gtatcttga ttactccaaa tggacagtc atgacacatg 2000  
 gggcgtaaa agtgccgata gctgtgctca gtgatggtac gttaaatttc 2050  
 acaaagttaa ctgtgcaaga tacaggcatg tacacatgta tggtgagtaa 2100  
 ttccgttggg aatactactg cttcagccac cctgaatgtt actgcagcaa 2150  
 ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200  
 ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtcccactcc 2250  
 agtggtcgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300  
 gcacaaggtc gacagagaaa accttcacca tcccagtgac tgatataaac 2350  
 agtgggatcc caggaattga tgaggtcatg aagactacca aaatcatcat 2400  
 tgggtgtttt gtggccatca cactcatggc tgcagtgatg ctggtcattt 2450  
 tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaca 2500  
 aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550



	155		160		165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly	170		175		180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly	185		190		195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg	200		205		210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp	215		220		225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln	230		235		240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile	245		250		255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val	260		265		270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp	275		280		285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His	290		295		300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp	305		310		315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys	320		325		330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp	335		340		345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro	350		355		360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys	365		370		375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn	380		385		390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val	395		400		405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp	410		415		420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr  
 425 430 435  
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
 440 445 450  
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
 455 460 465  
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
 470 475 480  
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
 485 490 495  
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
 500 505 510  
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
 515 520 525  
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala  
 530 535 540  
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
 545 550 555  
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
 560 565 570  
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
 575 580 585  
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
 590 595 600  
 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
 605 610 615  
 Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
 620 625 630  
 Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
 635 640

<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

agccgacgct gctcaagctg caactctgtt gcagttggca gttcttttcg 50



gtttccctcc tgctgtttgg gggcatgaaa gggcttcgcc gccgggagta 100  
 aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150  
 gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200  
 gcgcggctg ggagcttcgg gtagagacct aggcgcgtgg accgcgatga 250  
 gcgcgccgag cctccgtgcg cgcgcgcggg gggtggggct gctgctgtgc 300  
 gcggtgctgg ggcgcgctgg ccggtccgac agcggcggtc gcggggaact 350  
 cgggcagccc tctggggtag ccgcgcgagc cccatgcccc actacctgcc 400  
 gctgcctcgg ggacctgctg gactgcagtc gtaagcggct agcgcgtctt 450  
 cccgagccac tcccgctctg ggctcgtcgg ctggacttaa gtcacaacag 500  
 attatctttc atcaaggcaa gttccatgag ccaccttcaa agccttcgag 550  
 aagtgaaact gaacaacaat gaattggaga ccattccaaa tctgggacca 600  
 gtctcggcaa atattacact tctctccttg gctggaaaca ggattgttga 650  
 aatactccct gaacatctga aagagtttca gtcccttgaa actttggacc 700  
 ttagcagcaa caatatttca gagtccaaa ctgcatttcc agccctacag 750  
 ctcaaatact tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800  
 gtattttgac aatttgcca acacactcct tgtgttaaag ctgaacagga 850  
 accgaatctc agctatccca cccaagatgt ttaaactgcc ccaactgcaa 900  
 catctcgaat tgaaccgaaa caagattaaa aatgtagatg gactgacatt 950  
 ccaaggcctt ggtgctctga agtctctgaa aatgcaaaga aatggagtaa 1000  
 cgaaacttat ggatggagct ttttgggggc tgagcaacat ggaaattttg 1050  
 cagctggacc ataacaacct aacagagatt accaaaggct ggctttacgg 1100  
 cttgctgatg ctgcaggaac ttcattctcag ccaaaatgcc atcaacagga 1150  
 tcagccctga tgccctgggag ttctgccaga agctcagtga gctggaccta 1200  
 actttcaatc acttatcaag gttagatgat tcaagcttcc ttggcctaag 1250  
 cttactaaat aactgcaca ttgggaacaa cagagtcagc tacattgctg 1300  
 attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350

aatgaaattt cctggactat tgaagacatg aatgggtgctt tctctgggct 1400  
tgacaaactg aggcgactga tactccaagg aaatcggatc cgttctatta 1450  
ctaaaaaagc cttcactggt ttggatgcat tggagcatct agacctgagt 1500  
gacaacgcaa tcatgtcttt acaaggcaat gcattttcac aaatgaagaa 1550  
actgcaacaa ttgcatttaa atacatcaag ccttttgtgc gattgccagc 1600  
taaaatggct cccacagtgg gtggcgga aaactttca gagctttgta 1650  
aatgccagtt gtgcccattc tcagctgcta aaaggaagaa gcatttttgc 1700  
tgttagccca gatggctttg tgtgtgatga ttttcccaa cccagatca 1750  
cggttcagcc agaaacacag tcggcaataa aaggttccaa tttgagtttc 1800  
atctgctcag ctgccagcag cagtgattcc ccaatgactt ttgcttgga 1850  
aaaagacaat gaactactgc atgatgctga aatggaaaat tatgcacacc 1900  
tccgggcccc aggtggcgag gtgatggagt ataccaccat ccttcggctg 1950  
cgcgagggtg aatttgccag tgaggggaaa tatcagtgtg tcatctccaa 2000  
tcactttggt tcatcctact ctgtcaaagc caagcttaca gtaaatatgc 2050  
ttccctcatt caccaagacc cccatggatc tcaccatccg agctggggcc 2100  
atggcacgct tggagtgtgc tgctgtgggg caccagccc cccagatagc 2150  
ctggcagaag gatgggggca cagacttccc agctgcacgg gagagacgca 2200  
tgcatgtgat gcccaggat gacgtgttct ttatcgtgga tgtgaagata 2250  
gaggacattg gggatatacag ctgcacagct cagaacagtg caggaagtat 2300  
ttcagcaaat gcaactctga ctgtcctaga aacaccatca tttttgcggc 2350  
cactgttgga ccgaactgta accaaggag aaacagccgt cctacagtgc 2400  
attgctggag gaagccctcc ccctaaactg aactggacca aagatgatag 2450  
cccattggtg gtaaccgaga ggcacttttt tgcagcaggc aatcagcttc 2500  
tgattattgt ggactcagat gtcagtgatg ctgggaaata cacatgtgag 2550  
atgtctaaca ccctggcac tgagagagga aacgtgcgcc tcagtgtgat 2600  
ccccactcca acctgcgact ccctcagat gacagcccca tcgttagacg 2650  
atgacggatg ggccactgtg ggtgtcgtga tcatagccgt gggttgcgtg 2700



tttaataaaa tgtgtcaatt tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4050

aaa 4053

<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

Met Ser Ala Pro Ser Leu Arg Ala Arg Ala Ala Gly Leu Gly Leu  
1 5 10 15

Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly  
20 25 30

Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg  
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys  
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

090315.04004

				215						220					225
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr		Phe	Gln	Gly	Leu	Gly	Ala
				230						235					240
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn		Gly	Val	Thr	Lys	Leu	Met
				245						250					255
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn		Met	Glu	Ile	Leu	Gln	Leu
				260						265					270
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr		Lys	Gly	Trp	Leu	Tyr	Gly
				275						280					285
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu		Ser	Gln	Asn	Ala	Ile	Asn
				290						295					300
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe		Cys	Gln	Lys	Leu	Ser	Glu
				305						310					315
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser		Arg	Leu	Asp	Asp	Ser	Ser
				320						325					330
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr		Leu	His	Ile	Gly	Asn	Asn
				335						340					345
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala		Phe	Arg	Gly	Leu	Ser	Ser
				350						355					360
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn		Glu	Ile	Ser	Trp	Thr	Ile
				365						370					375
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly		Leu	Asp	Lys	Leu	Arg	Arg
				380						385					390
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg		Ser	Ile	Thr	Lys	Lys	Ala
				395						400					405
Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His		Leu	Asp	Leu	Ser	Asp	Asn
				410						415					420
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala		Phe	Ser	Gln	Met	Lys	Lys
				425						430					435
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser		Ser	Leu	Leu	Cys	Asp	Cys
				440						445					450
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val		Ala	Glu	Asn	Asn	Phe	Gln
				455						460					465
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His		Pro	Gln	Leu	Leu	Lys	Gly
				470						475					480

Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp	
				485					490					495	
Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala	
				500					505					510	
Ile	Lys	Gly	Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser	
				515					520					525	
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu	
				530					535					540	
Leu	His	Asp	Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln	
				545					550					555	
Gly	Gly	Glu	Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu	
				560					565					570	
Val	Glu	Phe	Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn	
				575					580					585	
His	Phe	Gly	Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn	
				590					595					600	
Met	Leu	Pro	Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg	
				605					610					615	
Ala	Gly	Ala	Met	Ala	Arg	Leu	Glu	Cys	Ala	Ala	Val	Gly	His	Pro	
				620					625					630	
Ala	Pro	Gln	Ile	Ala	Trp	Gln	Lys	Asp	Gly	Gly	Thr	Asp	Phe	Pro	
				635					640					645	
Ala	Ala	Arg	Glu	Arg	Arg	Met	His	Val	Met	Pro	Glu	Asp	Asp	Val	
				650					655					660	
Phe	Phe	Ile	Val	Asp	Val	Lys	Ile	Glu	Asp	Ile	Gly	Val	Tyr	Ser	
				665					670					675	
Cys	Thr	Ala	Gln	Asn	Ser	Ala	Gly	Ser	Ile	Ser	Ala	Asn	Ala	Thr	
				680					685					690	
Leu	Thr	Val	Leu	Glu	Thr	Pro	Ser	Phe	Leu	Arg	Pro	Leu	Leu	Asp	
				695					700					705	
Arg	Thr	Val	Thr	Lys	Gly	Glu	Thr	Ala	Val	Leu	Gln	Cys	Ile	Ala	
				710					715					720	
Gly	Gly	Ser	Pro	Pro	Pro	Lys	Leu	Asn	Trp	Thr	Lys	Asp	Asp	Ser	
				725					730					735	
Pro	Leu	Val	Val	Thr	Glu	Arg	His	Phe	Phe	Ala	Ala	Gly	Asn	Gln	
				740					745					750	

Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr	
				755					760					765	
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val	
				770					775					780	
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met	
				785					790					795	
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val	
				800					805					810	
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val	
				815					820					825	
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys	
				830					835					840	
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro	
				845					850					855	
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly	
				860					865					870	
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser	
				875					880					885	
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr	
				890					895					900	
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr	
				905					910					915	
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr	
				920					925					930	
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His	
				935					940					945	
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr	
				950					955					960	
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His	
				965					970					975	
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp	
				980					985					990	
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn	
				995					1000					1005	
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu	

09602615 "074004

1010	1015	1020
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn		
1025	1030	1035
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu		
1040	1045	1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
1085	1090	1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro		
1100	1105	1110
Asn Phe Gln Ser Tyr Asp Leu Asp Thr		
1115		

&lt;210&gt; 295

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 295

ggaaccgaat ctcagcta 18

&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 296

cctaaactga actggacca 19

&lt;210&gt; 297

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe



<400> 297  
ggctggagac actgaacct 19

<210> 298  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 298  
acagctgcac agctcagaac agtg 24

<210> 299

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 299  
cattcccagt ataaaaattt tc 22

<210> 300  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 300  
gggtcttggt gaatgagg 18

<210> 301  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 301  
gtgcctctcg gttaccacca atgg 24

<210> 302  
<211> 50  
<212> DNA  
<213> Artificial Sequence



<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

ttagcagctg aggatgggca caac 24

<210> 308

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 308

actccaagga aatcggatcc gttc 24

<210> 309

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 309

gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310

<211> 3296

<212> DNA

<213> Homo Sapien

<400> 310

caaaacttgc gtcgcggaga gcgcccagct tgacttgaat ggaaggagcc 50

cgagcccgcg gagcgcagct gagactgggg gagcgcgttc ggctgtggg 100

gcgccgctcg gcgccggggc gcagcagggg aggggaagct gtggtctgcc 150

ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtggtc 200

ccgtccccta tccctccttt atatagaaac cttccacact ggggaaggcag 250

ggcgaggca ggagggtca tggtagcaa ggaggccggc tgatctgcag 300

gcgcacagca ttccgagttt acagatTTTT acagatacca aatggaaggc 350

gaggaggcag aacagcctgc ctggttccat cagccctggc gccagggcg 400

atctgactcg gcacccccctg caggcaccat ggcccagagc cgggtgctgc 450  
 tgctcctgct gctgctgccg ccacagctgc acctgggacc tgtgcttgcc 500  
 gtgagggccc caggatttgg ccgaagtggc ggccacagcc tgagccccga 550  
 agagaacgaa tttgcggagg aggagccggt gctggtactg agccctgagg 600  
 agcccgggcc tggcccagcc gcggtcagct gcccccgaga ctgtgcctgt 650  
 tcccaggagg gcgtcgtgga ctgtggcggt attgacctgc gtgagttccc 700  
 gggggacctg cctgagcaca ccaaccacct atctctgcag aacaaccagc 750  
 tggaaaagat ctaccctgag gagctctccc ggctgcaccg gctggagaca 800  
 ctgaacctgc aaaacaaccg cctgacttcc cgagggctcc cagagaaggc 850  
 gtttgagcat ctgaccaacc tcaattacct gtacttggcc aataacaagc 900  
 tgaccttggc accccgcttc ctgccaaaag ccctgatcag tgtggacttt 950  
 gctgccaact atctcaccaa gatctatggg ctcacctttg gccagaagcc 1000  
 aaacttgagg tctgtgtacc tgcacaacaa caagctggca gacgcggggc 1050  
 tgccggacaa catgttcaac ggtccagca acgtcgaggt cctcatcctg 1100  
 tccagcaact tcctgcgcca cgtgccaag cacctgccgc ctgccctgta 1150  
 caagctgcac ctcaagaaca acaagctgga gaagatcccc ccgggggcct 1200  
 tcagcgagct gagcagcctg cgcgagctat acctgcagaa caactacctg 1250  
 actgacgagg gcctggacaa cgagaccttc tggaagctct ccagcctgga 1300  
 gtacctggat ctgtccagca acaacctgtc tcgggtccca gctgggctgc 1350  
 cgcgcagcct ggtgctgctg cacttggaaga agaacgccat ccggagcgtg 1400  
 gacgcgaatg tgctgacccc catccgcagc ctggagtacc tgctgctgca 1450  
 cagcaaccag ctgcgggagc agggcatcca cccactggcc ttccagggcc 1500  
 tcaagcgggt gcacacggtg cacctgtaca acaacgcgct ggagcgcgtg 1550  
 cccagtggcc tgccctgcgc cgtgcgaccc ctcatgatcc tgcacaacca 1600  
 gatcacaggc attggccgcg aagactttgc caccacctac ttcttgagg 1650  
 agctcaacct cagctacaac cgcataacca gccacaggt gcaccgcgac 1700

gccttcgcga agctgcgcct gctgcgctcg ctggacctgt cgggcaaccg 1750  
 gctgcacacg ctgccacctg ggctgcctcg aaatgtccat gtgctgaagg 1800  
 tcaagcgcaa tgagctggct gccttggcac gaggggcgct ggcgggcatg 1850  
 gctcagctgc gtgagctgta cctcaccagc aaccgactgc gcagccgagc 1900  
 cctggggcccc cgtgcctggg tggacctcgc ccatctgcag ctgctggaca 1950  
 tcgcccggaa tcagctcaca gagatccccg aggggctccc cgagtcaactt 2000  
 gagtacctgt acctgcagaa caacaagatt agtgcggtgc ccgccaatgc 2050  
 cttcgactcc acgcccacc tcaaggggat ctttctcagg tttacaagc 2100  
 tggtgtggg ctccgtggtg gacagtgcct tccggaggct gaagcacctg 2150  
 caggtcttgg acattgaagg caacttagag tttggtgaca tttccaagga 2200  
 ccgtggccgc ttggggaagg aaaaggagga ggaggaagag gaggaggagg 2250  
 aggaagagga aacaagatag tgacaagggt atgcagatgt gacctaggat 2300  
 gatggaccgc cggactcttt tctgcagcac acgcctgtgt gctgtgagcc 2350  
 cccactctg ccgtgctcac acagacacac ccagctgcac acatgaggca 2400  
 tcccacatga cacgggctga cacagtctca tatccccacc cttcccacg 2450  
 gcgtgtccca cggccagaca catgcacaca catcacacc tcaaacaccc 2500  
 agctcagcca cacacaacta ccctccaaac caccacagtc tctgtcacac 2550  
 cccactacc gctgccacgc cctctgaatc atgcaggga gggctctgcc 2600  
 ctgccctggc acacacaggc acccattccc tccccctgct gacatgtgta 2650  
 tgcgtatgca tacacaccac acacacacac atgcacaagt catgtgcaa 2700  
 cagccctcca aagcctatgc cacagacagc tcttgcccca gccagaatca 2750  
 gccatagcag ctgcgcgtct gccctgtcca tctgtccgtc cgttccctgg 2800  
 agaagacaca agggatatca tgctctgtgg ccagggtgct gccaccctct 2850  
 ggaactcaca aaagctggct tttattcctt tccatccta tggggacagg 2900  
 agccttcagg actgctggcc tggectggcc caccctgctc ctccagggtgc 2950  
 tgggcagtca ctctgctaag agtccctccc tgccacgccc tggcaggaca 3000  
 caggcacttt tccaatgggc aagcccagtg gaggcaggat gggagagccc 3050

cctgggtgct gctggggcct tggggcagga gtgaagcaga ggtgatggg 3100  
 ctgggctgag ccagggagga aggaccagc tgcacctagg agacacctt 3150  
 gttcttcagg cctgtggggg aagttccggg tgcctttatt ttttattctt 3200  
 ttctaaggaa aaaaatgata aaaatctcaa agctgatttt tcttggtata 3250  
 gaaaaactaa tataaaagca ttatccctat ccctgcaaaa aaaaaa 3296

<210> 311

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 311

gcattggccg cgagactttg cc 22

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 312

gcggccacgg tccttgaaa tg 22

<210> 313

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 313

tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314

<211> 3003

<212> DNA

<213> Homo Sapien

<400> 314

gggagggggc tccggggcgc gcgcagcaga cctgctccgg ccgcgcgcct 50

cgccgctgtc ctccgggagc ggcagcagta gcccgggcgg cgagggctgg 100

gggttcctcg agactctcag agggggcgct cccatcggcg cccaccaccc 150  
 caacctgttc ctgcgcgcgc actgcgcgtgc gcccaggac ccgctgcca 200  
 acatggattt tctcctggcg ctgggtgctgg tatcctcgt ctacctgcag 250  
 gcggccgcgc agttcgacgc gaggtggccc aggcaaatac tgatcatgat 300  
 tggcctatgt cggttatggtg ggaggattga ctgctgctgg ggctgggctc 350  
 gccagtcttg gggacagtgt cagcctgtgt gccaaaccgc atgcaaaca 400  
 ggtgaatgta tcggggccaaa caagtgcagc tgatcatcctg gttatgctgg 450  
 aaaaacctgt aatcaagatc taaatgagtg tggcctgaag ccccgccct 500  
 gtaagcacag gtgcatgaac acttacggca gctacaagt ctactgtctc 550  
 aacggatata tgctcatgcc ggatgggtcc tgctcaagt ccctgacctg 600  
 ctccatggca aactgtcagt atggctgtga tgttgtaaa ggacaaatac 650  
 ggtgccagt cccatcccct ggctgcacc tggctcctga tgggaggacc 700  
 tgtgtagatg ttgatgaatg tgctacagga agagcctct gccctagatt 750  
 taggcaatgt gtcaaacact ttgggagcta catctgcaag tgcatataag 800  
 gcttcgatct catgtatatt ggaggcaaat atcaatgtca tgacatagac 850  
 gaatgctcac ttggtcagta tcagtgcagc agctttgctc gatgttataa 900  
 cgtacgtggg tcctacaagt gcaaatgtaa agaaggatac cagggtgatg 950  
 gactgacttg tgtgtatata ccaaaagtta tgattgaacc ttcaggtcca 1000  
 attcatgtac caaagggaat tggtaccatt ttaaagggtg acacaggaaa 1050  
 taataattgg attcctgatg ttggaagtac ttggtggcct ccgaagacac 1100  
 catatatctc tcctatcatt accaacaggc ctacttctaa gccacaaca 1150  
 agacctacac caaagccaac accaattcct actccaccac caccaccac 1200  
 cctgccaca gagctcagaa cacctctacc acctacaacc ccagaaaggc 1250  
 caaccaccgg actgacaact atagcaccag ctgccagtac acctccagga 1300  
 gggattacag ttgacaacag ggtacagaca gaccctcaga aaccagagg 1350  
 agatgtgttc agtgttctgg tacacagttg taattttgac catggacttt 1400

gtggatggat cagggagaaa gacaatgact tgcactggga accaatcagg 1450  
 gaccagcag gtggacaata tctgacagtg tcggcagcca aagccccagg 1500  
 gggaaaagct gcacgcttgg tgctacctct cggccgcctc atgcattcag 1550  
 gggacctgtg cctgtcattc aggcacaagg tgacggggct gcactctggc 1600  
 aactccagg tgtttgtgag aaaacacggt gccacaggag cagccctgtg 1650  
 gggagaaat ggtggccatg gctggaggca aacacagatc accttgcgag 1700  
 gggctgacat caagagcgaa tcacaaagat gattaaagg ttggaaaaaa 1750  
 agatctatga tggaaaatta aaggaaactgg gattattgag cctggagaag 1800  
 agaagactga ggggcaaacc attgatggtt ttcaagtata tgaagggttg 1850  
 gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900  
 caagaggaaa ctggcttaga ctagagtata agggagcatt tcttggcagg 1950  
 ggccattgtt agaatacttc ataaaaaaag aagtgtgaaa atctcagtat 2000  
 ctctctctct ttctaaaaaa ttagataaaa atttgtctat ttaagatggt 2050  
 taaagatggt cttaccaag gaaaagtaac aaattataga atttcccaa 2100  
 agatgttttg atcctactag tagtatgcag tgaaaatctt tagaactaaa 2150  
 taatttggac aaggcttaat ttaggcattt ccctcttgac ctctaattgg 2200  
 agagggattg aaaggggaag agcccaccaa atgctgagct cactgaaata 2250  
 tctctccctt atggcaatcc tagcagtatt aaagaaaaaa ggaaactatt 2300  
 tattccaaat gagagtatga tggacagata ttttagtatc tcagtaatgt 2350  
 cctagtgtgg cgggtggttt caatgtttct tcatggtaaa ggtataagcc 2400  
 tttcatttgt tcaatggatg atgtttcaga tttttttttt tttaagagat 2450  
 ccttcaagga acacagttca gagagatttt catcgggtgc attctctctg 2500  
 ctctgtgtgt gacaagttat cttggctgct gagaaagagt gccctgcccc 2550  
 acaccggcag acctttcctt cacctcatca gtatgattca gtttctctta 2600  
 tcaattggac tctcccagg tccacagaac agtaatat tttgaacaat 2650  
 aggtacaata gaaggtcttc tgtcatttaa cctggtaaag gcagggctgg 2700  
 agggggaaaa taaatcatta agcctttgag taacggcaga atatatggct 2750



gtagatccat ttttaatggt tcatttcctt tatgggcata taactgcaca 2800  
 gctgaagatg aaaggggaaa ataaatgaaa attttacttt tcgatgccaa 2850  
 tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900  
 catcttggtt attatttaat gttttctaaa ataaaaaatg ttagtggttt 2950  
 tccaaatggc ctaataaaaa caattatttg taaataaaaa cactgttagt 3000  
 aat 3003

<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

Met	Asp	Phe	Leu	Leu	Ala	Leu	Val	Leu	Val	Ser	Ser	Leu	Tyr	Leu	1	5	10	15
Gln	Ala	Ala	Ala	Glu	Phe	Asp	Gly	Arg	Trp	Pro	Arg	Gln	Ile	Val	20	25	30	
Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys	35	40	45	
Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	50	55	60	
Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	65	70	75	
Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	80	85	90	
Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met	95	100	105	
Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met	110	115	120	
Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met	125	130	135	
Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg	140	145	150	
Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg	155	160	165	

09903615 "074004

Thr	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	Thr	Gly	Arg	Ala	Ser	Cys	
									175						180
Pro	Arg	Phe	Arg	Gln	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Ile	Cys	
									190						195
Lys	Cys	His	Lys	Gly	Phe	Asp	Leu	Met	Tyr	Ile	Gly	Gly	Lys	Tyr	
									205						210
Gln	Cys	His	Asp	Ile	Asp	Glu	Cys	Ser	Leu	Gly	Gln	Tyr	Gln	Cys	
									220						225
Ser	Ser	Phe	Ala	Arg	Cys	Tyr	Asn	Val	Arg	Gly	Ser	Tyr	Lys	Cys	
									235						240
Lys	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Asp	Gly	Leu	Thr	Cys	Val	Tyr	
									250						255
Ile	Pro	Lys	Val	Met	Ile	Glu	Pro	Ser	Gly	Pro	Ile	His	Val	Pro	
									265						270
Lys	Gly	Asn	Gly	Thr	Ile	Leu	Lys	Gly	Asp	Thr	Gly	Asn	Asn	Asn	
									280						285
Trp	Ile	Pro	Asp	Val	Gly	Ser	Thr	Trp	Trp	Pro	Pro	Lys	Thr	Pro	
									295						300
Tyr	Ile	Pro	Pro	Ile	Ile	Thr	Asn	Arg	Pro	Thr	Ser	Lys	Pro	Thr	
									310						315
Thr	Arg	Pro	Thr	Pro	Lys	Pro	Thr	Pro	Ile	Pro	Thr	Pro	Pro	Pro	
									325						330
Pro	Pro	Pro	Leu	Pro	Thr	Glu	Leu	Arg	Thr	Pro	Leu	Pro	Pro	Thr	
									340						345
Thr	Pro	Glu	Arg	Pro	Thr	Thr	Gly	Leu	Thr	Thr	Ile	Ala	Pro	Ala	
									355						360
Ala	Ser	Thr	Pro	Pro	Gly	Gly	Ile	Thr	Val	Asp	Asn	Arg	Val	Gln	
									370						375
Thr	Asp	Pro	Gln	Lys	Pro	Arg	Gly	Asp	Val	Phe	Ser	Val	Leu	Val	
									385						390
His	Ser	Cys	Asn	Phe	Asp	His	Gly	Leu	Cys	Gly	Trp	Ile	Arg	Glu	
									400						405
Lys	Asp	Asn	Asp	Leu	His	Trp	Glu	Pro	Ile	Arg	Asp	Pro	Ala	Gly	
									415						420
Gly	Gln	Tyr	Leu	Thr	Val	Ser	Ala	Ala	Lys	Ala	Pro	Gly	Gly	Lys	

	425		430		435
Ala	Ala	Arg	Leu	Val	Leu
			Pro	Leu	Gly
				Arg	Leu
				Met	His
				Ser	Gly
	440		445		450
Asp	Leu	Cys	Leu	Ser	Phe
				Arg	His
				Lys	Val
				Thr	Gly
				Leu	His
				Ser	
	455		460		465
Gly	Thr	Leu	Gln	Val	Phe
				Val	Arg
				Lys	His
				Gly	Ala
				His	Gly
				Ala	
	470		475		480
Ala	Leu	Trp	Gly	Arg	Asn
				Gly	Gly
				His	Gly
				Trp	Arg
				Gln	Thr
				Gln	
	485		490		495
Ile	Thr	Leu	Arg	Gly	Ala
				Asp	Ile
				Lys	Ser
				Glu	Ser
				Gln	Arg
	500		505		

<210> 316

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 316

gatggttcct gctcaagtgc cctg 24

<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 317

ttgcacttgt aggacccacg tacg 24

<210> 318

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 318

ctgatgggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319

<211> 2110

<212> DNA

090916.0404

<213> Homo Sapien

<400> 319

```

cttctttgaa aaggattatc acctgatcag gttctctctg catttgcccc 50

tttagattgt gaaatgtggc tcaaggtctt cacaactttc ctttcctttg 100

caacaggtgc ttgctcgggg ctgaaggtga cagtgccatc acacactgtc 150

catggcgta gaggtcaggc cctctaccta cccgtccact atggcttcca 200

cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250

caatgcccac atacttactg ggctctgtga ataagtctgt ggttcctgac 300

ttggaatacc aacacaagtt caccatgatg ccacccaatg catctctgct 350

tatcaaccca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400

acattcaggg aatggaact ctatctgcca gtcagaagat acaagtcacg 450

gttgatgatc ctgtcacaaa gccagtgggtg cagattcatc ctccctctgg 500

ggctgtggag tatgtgggga acatgaccct gacatgccat gtggaagggg 550

gcactcggct agcttaccaa tggctaaaaa atgggagacc tgtccacacc 600

agctccacct actccttttc tccccaaaac aatacccttc atattgctcc 650

agtaaccaag gaagacattg ggaattacag ctgcctgggtg aggaaccctg 700

tcagtgaat ggaaagtgat atcattatgc ccatcatata ttatggacct 750

tatggacttc aagtgaattc tgataaaggg ctaaaagtag ggggaagtgtt 800

tactgttgac cttggagagg ccacacctatt tgattgttct gctgattctc 850

atccccccaa cacctactcc tggattagga ggactgacaa tactacatat 900

atcattaagc atgggcctcg cttagaagtt gcattctgaga aagtagccca 950

gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000

aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050

cttgacacaga aaggaaaatc attgtcacct ttagcaagta taactggaat 1100

atcactattt ttgattatat ccattgtgtct tctcttctta tggaaaaaat 1150

atcaacccta caaagttata aaacagaaac tagaaggcag gccagaaaca 1200

gaatacagga aagctcaaac attttcaggc catgaagatg ctctggatga 1250

```

cttcggaata tatgaatttg ttgcttttcc agatgtttct ggtgtttcca 1300  
 ggattccaag caggtctgtt ccagcctctg attgtgtatc ggggcaagat 1350  
 ttgcacagta cagtgtatga agttattcag cacatccctg cccagcagca 1400  
 agaccatcca gagtgaactt tcatgggcta aacagtacat tcgagtgaaa 1450  
 ttctgaagaa acattttaag gaaaaacagt ggaaaagtat attaactctgg 1500  
 aatcagtgaa gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550  
 tgcagaatag aggcatttat gcaaattgaa ctgcaggttt ttcagcatat 1600  
 acacaatgtc ttgtgcaaca gaaaaacatg ttgggggaaat attcctcagt 1650  
 ggagagtcgt tctcatgctg acggggagaa cgaaagtgc aggggtttcc 1700  
 tcataagttt tgtatgaaat atctctacaa acctcaatta gttctactct 1750  
 acactttcac tatcatcaac actgagacta tctgtctca cctacaaatg 1800  
 tggaaacttt acattgttcg atttttcagc agactttgtt ttattaaatt 1850  
 tttattagtg ttaagaatgc taaatttatg tttcaatttt atttccaaat 1900  
 ttctatcttg ttatttgtac aacaaagtaa taaggatggt tgtcacaaaa 1950  
 aaaaaactat gccttctctt ttttttcaat caccagtagt atttttgaga 2000  
 agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050  
 tttcaaggaa agatggattc aaataaatta ttctgttttt gcttttaaaa 2100  
 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met	Trp	Leu	Lys	Val	Phe	Thr	Thr	Phe	Leu	Ser	Phe	Ala	Thr	Gly
1				5					10					15

Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
				20					25					30

Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35					40					45

His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50					55					60

Pro	His	Thr	Met	Pro	Lys	Tyr	Leu	Leu	Gly	Ser	Val	Asn	Lys	Ser	
				65					70					75	
Val	Val	Pro	Asp	Leu	Glu	Tyr	Gln	His	Lys	Phe	Thr	Met	Met	Pro	
				80					85					90	
Pro	Asn	Ala	Ser	Leu	Leu	Ile	Asn	Pro	Leu	Gln	Phe	Pro	Asp	Glu	
				95					100					105	
Gly	Asn	Tyr	Ile	Val	Lys	Val	Asn	Ile	Gln	Gly	Asn	Gly	Thr	Leu	
				110					115					120	
Ser	Ala	Ser	Gln	Lys	Ile	Gln	Val	Thr	Val	Asp	Asp	Pro	Val	Thr	
				125					130					135	
Lys	Pro	Val	Val	Gln	Ile	His	Pro	Pro	Ser	Gly	Ala	Val	Glu	Tyr	
				140					145					150	
Val	Gly	Asn	Met	Thr	Leu	Thr	Cys	His	Val	Glu	Gly	Gly	Thr	Arg	
				155					160					165	
Leu	Ala	Tyr	Gln	Trp	Leu	Lys	Asn	Gly	Arg	Pro	Val	His	Thr	Ser	
				170					175					180	
Ser	Thr	Tyr	Ser	Phe	Ser	Pro	Gln	Asn	Asn	Thr	Leu	His	Ile	Ala	
				185					190					195	
Pro	Val	Thr	Lys	Glu	Asp	Ile	Gly	Asn	Tyr	Ser	Cys	Leu	Val	Arg	
				200					205					210	
Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile	
				215					220					225	
Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu	
				230					235					240	
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu	
				245					250					255	
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp	
				260					265					270	
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro	
				275					280					285	
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp	
				290					295					300	
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu	
				305					310					315	
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu	

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu		
440	445	450

&lt;210&gt; 321

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

gatcctgtca caaagccagt ggtgc 25

&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

cactgacagg gttcctcacc cagg 24

&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

gcaagcggcg	aaatggcgcc	ctccgggagt	cttgccagttc	ccctggcagt	50
cctggtgctg	ttgctttggg	gtgctccctg	gacgcacggg	cggcggagca	100
acgttcgcgt	catcacggac	gagaactgga	gagaactgct	ggaaggagac	150
tggatgatag	aattttatgc	cccgtggtgc	cctgcttgct	aaaatcttca	200
accggaatgg	gaaagttttg	ctgaatgggg	agaagatctt	gaggttaata	250
ttgcgaaagt	agatgtcaca	gagcagccag	gactgagtgg	acggtttatc	300
ataactgctc	ttcctactat	ttatcattgt	aaagatgggtg	aatttaggcg	350
ctatcagggg	ccaaggacta	agaaggactt	cataaaacttt	ataagtgata	400
aagagtggaa	gagtattgag	cccgtttcat	catggtttgg	tccaggttct	450
gttctgatga	gtagtatgtc	agcactcttt	cagctatcta	tgtggatcag	500
gacgtgccat	aactacttta	ttgaagacct	tggattgcca	gtgtggggat	550
catatactgt	ttttgcttta	gcaactctgt	tttccggact	gttattagga	600
ctctgtatga	tattttgtggc	agattgcctt	tgtccttcaa	aaaggcgcag	650
accacagcca	taccataacc	cttcaaaaaa	attattatca	gaatctgcac	700
aacctttgaa	aaaagtggag	gaggaacaag	aggcggatga	agaagatgtt	750
tcagaagaag	aagctgaaag	taaagaagga	acaaacaaag	actttccaca	800
gaatgccata	agacaacgct	ctctgggtcc	atcattggcc	acagataaat	850
cctagttaaa	ttttatagtt	atcttaatat	tatgattttg	ataaaaacag	900
aagattgatc	attttgtttg	gtttgaagtg	aactgtgact	tttttgaata	950
ttqcaqqgtt	cagtctagat	tgtcattaaa	ttgaagagtc	tacattcaga	1000



acataaaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050  
 gatgggttttaa atagttctct aatttttgaa aaatcgtgcc aagcaataag 1100  
 atttatgtat atttggttaa taataaccta tttcaagtct gagttttgaa 1150  
 aatttacatt tcccaagtat tgcattattg aggtatttaa gaagattatt 1200  
 ttagagaaaa atatttctca tttgatataa ttttctctg tttcactgtg 1250  
 tgaaaaaaag aagatatttc ccataaatgg gaagtttgcc cattgtctca 1300  
 agaaatgtgt atttcagtga caatttcgtg gtcttttttag aggtatattc 1350  
 caaaatttcc ttgtattttt aggttatgca actaataaaa actaccttac 1400  
 attaattaat tacagttttc tacacatggg aatacaggat atgctactga 1450  
 tttaggaagt ttttaagttc atgggtattct cttgattcca acaaagtttg 1500  
 attttctctt gtatttttct tacttactat gggttacatt ttttattttt 1550  
 caaattggat gataatttct tggaaacatt ttttatgttt tagtaaacag 1600  
 tatttttttg ttgtttcaaa ctgaagttta ctgagagatc catcaaattg 1650  
 aacaatctgt tgtaatttaa aattttggcc acttttttca gattttacat 1700  
 cattcttgct gaacttcaac ttgaaattgt ttttttttc tttttggatg 1750  
 tgaaggtgaa cattcctgat ttttgtctga tgtgaaaaag ccttgggtatt 1800  
 ttacattttg aaaattcaaa gaagcttaat ataaaagttt gcattctact 1850  
 caggaaaaag catcttcttg tatatgtctt aaatgtattt ttgtcctcat 1900  
 atacagaaag ttcttaattg attttacagt ctgtaatgct tgatgtttta 1950  
 aaataataac atttttatat tttttaaaag acaaacttca tattatcctg 2000  
 tgttctttcc tgactggtaa tattgtgtgg gatttcacag gtaaaagtca 2050  
 gtaggatgga acattttagt gtatttttac tccttaaaga gctagaatac 2100  
 atagttttca ccttaaaaga agggggaaaa tcataaatac aatgaatcaa 2150  
 ctgaccatta cgtagtagac aatttctgta atgtccctt ctttctaggc 2200  
 tctgttgctg tgtgaatcca ttagatttac agtatcgtaa tatacaagtt 2250  
 ttcttttaaag cctctcctt tagaatttaa aatattgtac cattaaagag 2300  
 tttggatgtg taacttgtga tgccttagaa aaatatccta agcacaaaat 2350

<210> 325

&lt;212&gt; PRT

<400> 325

Met	Ala	Pro	Ser	Gly	Ser	Leu	Ala	Val	Pro	Leu	Ala	Val	Leu	Val
1				5					10					15
Leu	Leu	Leu	Trp	Gly	Ala	Pro	Trp	Thr	His	Gly	Arg	Arg	Ser	Asn
				20					25					30
Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly
				35					40					45
Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln
				50					55					60
Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp
				65					70					75
Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly
				80					85					90
Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His
				95					100					105
Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys
				110					115					120
Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile
				125					130					135
Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser
				140					145					150
Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys
				155					160					165
His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser
				170					175					180
Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu
				185					190					195
Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	Ser	Lys
				200					205					210
Arg	Arg	Arg	Pro	Gln	Pro	Tyr	Pro	Tyr	Pro	Ser	Lys	Lys	Leu	Leu



<220>

<223> Synthetic Oligonucleotide Probe

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttcccctg gcagtcctgg tgctgttgct ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

gcgagtgtcc agctgctggag acccgtgata attcgttaac taattcaaca 50

aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccacagtg 100

ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150

acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200

ggtttgggtgt cctgagctgt gtgcaggcgc aattcttcac ctctattggg 250

cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300

agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350

ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400

tacctggctc accctgtgaa tgcctacaaa ctggtgaagc ggctaaacac 450

agactggcct gcgctggagg accttgtcct gcaggactca gctgcagggt 500

ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550

gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600

ggaccacaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650

caatgctgag tgtggatgac tgctttggga tgggccgctc ggctacaat 700

gaaggggact attatcatatc ggtgttgtgg atggagcagg tgctaaagca 750

gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800  
acctcagcta tgctgtcttc cagttgggtg atctgcaccg tgccctggag 850  
ctcaccgcgc gcctgtcttc ccttgaccca agccacgaac gagctggagg 900  
gaatctgcgg tactttgagc agttattgga ggaagagaga gaaaaaacgt 950  
taacaaatca gacagaagct gagctagcaa cccagaagg catctatgag 1000  
aggcctgtgg actacctgcc tgagagggat gtttacgaga gcctctgtcg 1050  
tggggagggg gtcaaaactga cccccgtag acagaagagg cttttctgta 1100  
ggtaccacca tggcaacagg gccccacagc tgctcattgc ccccttcaaa 1150  
gaggaggacg agtgggacag cccgcacatc gtcagggtact acgatgtcat 1200  
gtctgatgag gaaatcgaga ggatcaagga gatcgcaaaa cctaaacttg 1250  
cacgagccac cgttcgtgat cccaagacag gagtccctac tgtcgccagc 1300  
taccggggtt ccaaaagctc ctggctagag gaagatgatg accctgttgt 1350  
ggcccgagta aatcgtcgga tgcagcatat cacagggtta acagtaaaga 1400  
ctgcagaatt gttacagggt gcaaattatg gagtgggagg acagtatgaa 1450  
ccgcacttcg acttctctag gcgacctttt gacagcggcc tcaaaacaga 1500  
ggggaatagg ttagcgacgt ttcttaacta catgagtgat gtagaagctg 1550  
gtggtgccac cgtcttcctt gatctggggg ctgcaatttg gcctaagaag 1600  
ggtacagctg tgttctggta caacctcttg cggagcgggg aagggtgacta 1650  
ccgaacaaga catgtgcct gccctgtgct tgtgggctgc aagtgggtct 1700  
ccaataagtg gttccatgaa cgaggacagg agttcttgag accttggtga 1750  
tcaacagaag ttgactgaca tccttttctg tccttcccct tcctggctct 1800  
tcagcccatg tcaacgtgac agacaccttt gtatgttctt ttgtatgttc 1850  
ctatcaggct gatTTTTGGA gaaatgaatg tttgtctgga gcagaggagg 1900  
accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950  
gcctgtgcca tcctggccc caaggctagg atcaaagtgg ctgcagcaga 2000  
gtagctgtc tagcgcttag caagggtgct ttgtacctca ggtgttttag 2050  
gtgtgagatg tttcagtga ccaaagttct gataccttgt ttacatgttt 2100

gtttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met	Lys	Leu	Trp	Val	Ser	Ala	Leu	Leu	Met	Ala	Trp	Phe	Gly	Val	1	5	10	15
Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met	20	25	30	
Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys	35	40	45	
Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser	50	55	60	
Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp	65	70	75	
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val	80	85	90	
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu	95	100	105	
Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg	110	115	120	
Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala	125	130	135	
Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile	140	145	150	
Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser	155	160	165	
Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly	170	175	180	
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln	185	190	195	
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu	200	205	210	

09030645-07004



Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp  
530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

0902645-0404



<400> 336  
acactcagca ttgcctggta cttg 24

<210> 337  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 337  
gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338  
<211> 2789  
<212> DNA  
<213> Homo Sapien

<400> 338  
gcagtattga gttttacttc ctcctctttt tagtggaaga cagaccataa 50  
tcccagtggt agtgaaattg attgtttcat ttattaccgt tttggctggg 100  
ggttagttcc gacaccttca cagttgaaga gcaggcagaa ggagttgtga 150  
agacaggaca atcttcttgg ggatgctggg cctggaagcc agcgggcctt 200  
gctctgtctt tggcctcatt gacccaggt tctctggta aaactgaaag 250  
cctactactg gcctgggtgcc catcaatcca ttgatccttg aggctgtgcc 300  
cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350  
ttggctctgc tgcggccagc gcttccctc atcttagggc tgtctctggg 400  
gtgcagcctg agcctcctgc gggtttcctg gatccagggg gagggagaag 450  
atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500  
tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550  
cccctactac agggacccca acaagcccta caagaagggtg ctcaggactc 600  
ggtacatcca gacagagctg ggctcccgtg agcgggttgct ggtggctgtc 650  
ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700  
ggtggcccat cacttccctc ggttactcta cttcactggg cagcgggggg 750  
cccgggctcc agcagggatg caggtggtgt ctcatgggga tgagcggccc 800

gcctggctca tgtcagagac cctgcgccac cttcacacac actttggggc 850  
 cgactacgac tggttcttca tcatgcagga tgacacatat gtgcaggccc 900  
 cccgcctggc agcccttgct ggccacctca gcatcaacca agacctgtac 950  
 ttaggccggg cagaggagtt cattggcgca ggcgagcagg cccggtactg 1000  
 tcatgggggc tttggctacc tgttgtcacg gagtctcctg cttcgtctgc 1050  
 ggccacatct ggatggctgc cgaggagaca ttctcagtgc ccgtcctgac 1100  
 gagtggcttg gacgctgcct cattgactct ctgggcgtcg gctgtgtctc 1150  
 acagcaccag gggcagcagt atcgctcatt tgaactggcc aaaaataggg 1200  
 accctgagaa ggaagggagc tcggctttcc tgagtgcctt cgccgtgcac 1250  
 cctgtctccg aaggtaccct catgtaccgg ctccacaaac gcttcagcgc 1300  
 tctggagttg gagcgggctt acagtgaaat agaacaactg caggctcaga 1350  
 tccggaacct gaccgtgctg acccccgaag gggaggcagg gctgagctgg 1400  
 cccgttgggc tccttgcctc ttccacacca cactctcgtt ttgaggtgct 1450  
 gggctgggac tacttcacag agcagcacac cttctcctgt gcagatgggg 1500  
 ctccaagtgc ccactacag ggggctagca gggcggacgt ggggtgatgcg 1550  
 ttggagactg ccctggagca gctcaatcgg cgctatcagc cccgcctgcg 1600  
 cttccagaag cagcgactgc tcaacggcta tcggcgcttc gaccacgac 1650  
 ggggcatgga gtacaccctg gacctgctgt tggaatgtgt gacacagcgt 1700  
 gggcaccggc gggccctggc tcgcagggtc agcctgctgc ggccactgag 1750  
 ccgggtggaa atcctaccta tgccctatgt cactgaggcc acccgagtgc 1800  
 agctggtgct gccactcctg gtggctgaag ctgctgcagc cccggctttc 1850  
 ctcgaggcgt ttgcagccaa tgtcctggag ccacgagaac atgcattgct 1900  
 caccctgttg ctggtctacg ggccacgaga aggtggccgt ggagctccag 1950  
 acccatttct tgggggtgaag gctgcagcag cggagttaga gcgacgggtac 2000  
 cctgggacga ggctggcctg gctcgtctgt cgagcagagg ccccttccca 2050  
 ggtgcgactc atggacgtgg tctcgaagaa gcaccctgtg gacactctct 2100

tcttccttac caccgtgtgg acaaggcctg ggcccgaagt cctcaaccgc 2150  
 tgtcgcatga atgccatctc tggtcggcag gccttctttc cagtccattt 2200  
 ccaggagtgc aatcctgccc tgtcaccaca gagatcacc ccaggggccc 2250  
 cgggggctgg ccttgacccc cctccccctc ctggtgctga cccctcccg 2300  
 ggggctccta taggggggag atttgaccgg caggcttctg cggagggctg 2350  
 cttctacaac gctgactacc tggcggcccg agcccggtg gcaggatgaac 2400  
 tggcaggcca ggaagaggag gaagccctgg aggggctgga ggtgatggat 2450  
 gttttcctcc ggttctcagg gctccacctc tttcgggccg tagagccagg 2500  
 gctggtgcag aagttctccc tgcgagactg cagcccacgg ctcaagtgaag 2550  
 aactctacca ccgctgccgc ctcaagcaacc tggaggggct agggggccgt 2600  
 gccagctgg ctatggctct ctttgagcag gaggaggcca atagcactta 2650  
 gccgcctgg gggccctaac ctcaattacct ttctttgtc tgcctcagcc 2700  
 ccaggaaggg caaggcaaga tggcggacag atagagaatt gttgctgtat 2750  
 tttttaaata tgaaaatggt attaaacatg tcttctgcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met Arg Leu Ser Ser Leu Leu Ala Leu Leu Arg Pro Ala Leu Pro  
 1 5 10 15

Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg  
 20 25 30

Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala  
 35 40 45

Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg  
 50 55 60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr  
 65 70 75

Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg  
 80 85 90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

	95		100		105
Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val	110		115		120
Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr	125		130		135
Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser	140		145		150
His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg	155		160		165
His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile	170		175		180
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu	185		190		195
Ala Gly His Leu Ser Ile Asn Gln Asp Leu Tyr Leu Gly Arg Ala	200		205		210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg Tyr Cys His Gly	215		220		225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser Leu Leu Leu Arg Leu Arg	230		235		240
Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro	245		250		255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly	260		265		270
Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu	275		280		285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu	290		295		300
Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr	305		310		315
Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr	320		325		330
Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val	335		340		345
Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu	350		355		360

Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	365	370	375
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	380	385	390
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	395	400	405
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	410	415	420
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	425	430	435
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	440	445	450
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	455	460	465
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	470	475	480
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	485	490	495
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	500	505	510
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	515	520	525
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	530	535	540
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	545	550	555
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	560	565	570
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	575	580	585
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	590	595	600
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	605	610	615
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	620	625	630

09002645-071001

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
 740 745 750  
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
 755 760 765  
 Gln Glu Gln Ala Asn Ser Thr  
 770

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

cggagtgggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50  
 tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100  
 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350  
 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

```
<210> 341
<211> 318
<212> PRT
<213> Homo Sapien
```

&lt;400&gt; 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly	1	5	10	15
Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile	20	25	30	
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	35	40	45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg	50	55	60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val	65	70	75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	80	85	90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val	95	100	105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu	110	115	120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp	125	130	135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile	140	145	150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln	155	160	165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr	170	175	180	
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys	185	190	195	
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln	200	205	210	
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val	215	220	225	
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala	230	235	240	
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile	245	250	255	
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys				

09002615.071004



	260		265		270
Cys Ser Asp Met	Ala Val Thr Phe Asn Gly	Leu Thr Pro Asn Gln			
	275	280			285
Met His Val Met	Met Tyr Gly Val Tyr Arg	Leu Arg Ala Phe Gly			
	290	295			300
His Ile Phe Asn	Asp Ala Leu Val Phe Leu	Pro Pro Asn Gly Ser			
	305	310			315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaatgc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

090915 0400

<223> Synthetic Oligonucleotide Probe

<400> 345

gggtgtgatg cttggaagca ttttctgtgc ttgatcact atgctaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tgggtgtctca tgggg 25

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaatt acgactcact atagggctca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350

<211> 48

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 350  
ggattctaatac gactcact atagggcggc gatgtccact ggggctac 48

<210> 351  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 351  
ctatgaaatt aaccctcact aaaggacga ggaagatggg cggatggt 48

<210> 352  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 352  
ggattctaatac gactcact atagggcacc cacgcgtccg gctgctt 47

<210> 353  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 353  
ctatgaaatt aaccctcact aaaggacgg gggacaccac ggaccaga 48

<210> 354  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 354  
ggattctaatac gactcact atagggcttg ctgcggtttt tgttcctg 48

<210> 355  
<211> 48

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 355  
ctatgaaatt aaccctcact aaagggagct gccgatccca ctggtatt 48

<210> 356  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 356  
ggattctaatt acgactcact atagggcgga tcctggccgg cctctg 46

<210> 357  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 357  
ctatgaaatt aaccctcact aaagggagcc cgggcatggt ctcagtta 48

<210> 358  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 358  
ggattctaatt acgactcact atagggcggg aagatggcga ggaggag 47

<210> 359  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 359  
ctatgaaatt aaccctcact aaagggacca aggccacaaa cggaaatc 48

<210> 360  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 360  
ggattctaatac gactcact atagggtgt gctttcattc tgccagta 48

<210> 361  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 361  
ctatgaaatt aaccctcact aaaggagggt tacaattaag gggtagat 48

<210> 362  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 362  
ggattctaatac gactcact atagggtgtg cctcgctcct gctcctg 47

<210> 363  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 363  
ctatgaaatt aaccctcact aaaggaggga ttgccgcgac cctcacag 48

<210> 364  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 364

09902645-071004

ggatttctaatac gactcact atagggcccc tcctgccttc cctgtcc 47

<210> 365

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 365

ctatgaaatt aaccctcact aaagggagtg gtggccgcga ttatctgc 48

<210> 366

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 366

ggatttctaatac gactcact atagggcgca gcgatggcag cgatgagg 48

<210> 367

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 367

ctatgaaatt aaccctcact aaagggacag acggggcaga gggagtg 47

<210> 368

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 368

ggatttctaatac gactcact atagggccag gaggcgtgag gagaaac 47

<210> 369

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

"GTGCGCA"CGATGAGG

<223> Synthetic Oligonucleotide Probe

<400> 369

ctatgaaatt aaccctcact aaagggaaag acatgtcatc gggagtgg 48

<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370

ggattctaatacgcactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggattctaatacgcactcact atagggccag ggaaatccgg atgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

090616-0404

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 374  
 ggatttcta atcgactcact atagggccag ctacccgcag gaggagg 47

<210> 375  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 375  
 ctatgaaatt aaccctcact aaagggatcc caggtgatga ggtccaga 48

<210> 376  
 <211> 997  
 <212> DNA  
 <213> Homo Sapien

<400> 376  
 cccacgcgtc cgatcttacc aacaaaacac tcctgaggag aaagaaagag 50  
 agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100  
 aaaaaatgaa ttcattctaaa tcatctgaaa cacaatgcac agagagagga 150  
 tgcttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200  
 atttctcagt gcctgtttca tcaccagatg tgttgtgaca tttcgcatct 250  
 ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300  
 ctctcctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350  
 gaactgggaa tatttttcaat ccagctgcta cttcttttct actgacacca 400  
 tttcctgggc gttaagttaa aagaactgct cagccatggg ggctcacctg 450  
 gtgggttatca actcacagga ggagcaggaa ttccttttct acaagaaacc 500  
 taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgagggtc 550  
 agtggcaatg ggtggacggc acacctttga caaagtctct gagcttctgg 600  
 gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650  
 gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700  
 tcaattatatt tcggatttgt gaaatggtag gaataaatcc ttgaacaaa 750



```
<210> 377
<211> 219
<212> PRT
<213> Homo Sapien
```

<400> 377															
Met	Asn	Ser	Ser	Lys	Ser	Ser	Glu	Thr	Gln	Cys	Thr	Glu	Arg	Gly	
1				5					10					15	
Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro	
				20					25					30	
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr	
				35					40					45	
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro	
				50					55					60	
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser	
				65					70					75	
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser	
				80					85					90	
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu	
				95					100					105	
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser	
				110					115					120	
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	
				125					130					135	
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp	
				140					145					150	
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp	
				155					160					165	
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala	
				170					175					180	

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
 185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
 200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu  
 215

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

ttcagcttct gggatgtagg g 21

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

<210> 381

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

gcagattttg aggacagcca cctcca 26

```

<210> 382
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 382
    ggccttgccag acaaccgt 18

<210> 383
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 383
    cagactgagg gagatccgag a 21

<210> 384
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 384
    cagctgccct tccccaacca 20

<210> 385
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 385
    catcaagcgc ctctacca 18

<210> 386
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 386

```

<210> 387  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 387  
gggccatcac agctccct 18

<210> 388  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 388  
gggatgtggt gaacacagaa ca 22

<210> 389  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 389  
tgccagctgc atgctgccag tt 22

<210> 390  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 390  
cagaaggatg tcccgtggaa 20

<210> 391  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

gccgctgtcc actgcag 17

<210> 392

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

gacggcatcc tcagggccac a 21

<210> 393

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

atgtcctcca tgcccacgcg 20

<210> 394

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 394

gagtgcgaca tcgagagctt 20

<210> 395

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 395

ccgcagcctc agtgatga 18

<210> 396

<211> 21

<212> DNA

<213> Artificial Sequence

090616-074004

<220>  
<223> Synthetic oligonucleotide probe

<400> 396  
gaagagcaca gctgcagatc c 21

<210> 397  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 397  
gaggtgtcct ggctttggta gt 22

<210> 398  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 398  
cctctggcgc cccactcaa 20

<210> 399  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 399  
ccaggagagc tggcgatg 18

<210> 400  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 400  
gcaaattcag ggctcactag aga 23

<210> 401  
<211> 29

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 401  
cacagagcat ttgtccatca gcagttcag 29

<210> 402  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 402  
ggcagagact tccagtcact ga 22

<210> 403  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 403  
gccaaggggtg gtgtagata gg 22

<210> 404  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 404  
caggccccct tgatctgtac ccca 24

<210> 405  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 405  
gggacgtgct tctacaagaa cag 23

<210> 406  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 406  
caggcttaca atgttatgat cagaca 26  
  
<210> 407  
<211> 31  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 407  
tattcagagt tttccattgg cagtgccagt t 31  
  
<210> 408  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 408  
tctacatcag cctctctgcg c 21  
  
<210> 409  
<211> 23  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 409  
cgatcttctc caccagag cg 23  
  
<210> 410  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 410



gccaggcctc acattcgt 18

<210> 411

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

ctccctgaat ggcagcctga gca 23

<210> 412

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

aggtgtttat taaggccta cgct 24

<210> 413

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cagagcagag ggtgccttg 19

<210> 414

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 414

tggcggagtc ccctcttggc t 21

<210> 415

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 415

ccctgtttcc ctatgcatca ct 22

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

tcaaccctg accctttcct a 21

<210> 417

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

ggcaggggac aagccatctc tcct 24

<210> 418

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

gggactgaac tgccagcttc 20

<210> 419

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 419

gggccctaac ctcattacct tt 22

<210> 420

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 420

tgtctgcctc agccccagga agg 23

<210> 421

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

tctgtccacc atcttgccctt g 21

<210> 422

<211> 3554

<212> DNA

<213> Homo Sapien

<400> 422

```

gggactacaa gccgcgccgc gctgccgctg gcccctcagc aaccctcgac 50
atggcgctga ggcgccacc gcgactccgg ctctgcgctc ggctgcctga 100
cttcttctctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150
tcaaattccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200
ctgtcttgca tcattacgga ttgcagaca agtgacccca ggatcgagtg 250
gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300
ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350
aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400
cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450
ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500
ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550
ccggcctcac tacagctggg atcgcaatga tgtaccactg cccacggatt 600
ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650
acaggcactt tgggtgttcac tgctgttcac aaggacgact ctgggcagta 700
ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750

```

agatggaagt ctatgacctg aacattggcg gaattattgg gggggttctg 800  
 gttgtccttg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850  
 cagacgtggc tacttcatca acaataaaca ggatggagaa agttacaaga 900  
 acccagggaa accagatgga gttaactaca tccgcactga cgaggagggc 950  
 gacttcagac acaagtcatc gtttgtgatc tgagaccgcg ggtgtggctg 1000  
 agagcgcaca gagcgcacgt gcacatacct ctgctagaaa ctctgtcaa 1050  
 ggcagcgaga gctgatgcac tcggacagag ctagacactc attcagaagc 1100  
 ttttcgtttt ggccaaagt gaccactact cttcttactc taacaagcca 1150  
 catgaataga agaattttcc tcaagatgga cccggtaaat ataaccacaa 1200  
 ggaagcgaaa ctgggtgcgt tctactgagtt gggttcctaa tctgtttctg 1250  
 gcctgattcc cgcgatgagta ttaggggtgat cttaaagagt ttgctcacgt 1300  
 aaacgcccgt gctgggccct gtgaagccag catgttcacc actggctggt 1350  
 cagcagccac gacagcacca tgtgagatgg cgagggtggc ggacagcacc 1400  
 agcagcgcac cccggcggga acccagaaaa ggcttcttac acagcagcct 1450  
 tacttcatcg gccacagac accaccgcag tttcttctta aaggctctgc 1500  
 tgatcgggtg tgcatgtcc attgtggaga agctttttgg atcagcattt 1550  
 tgtaaaaaca accaaaatca ggaaggtaaa ttggttgctg gaagagggat 1600  
 cttgcctgag gaaccctgct tgtccaacag ggtgtcagga ttttaaggaaa 1650  
 accttcgtct taggctaagt ctgaaatggt actgaaatat gcttttctat 1700  
 gggctctggt tattttataa aattttacat cttaaatttt gctaaggatg 1750  
 tattttgatt attgaaaaga aaatttctat ttaaactgta aatatattgt 1800  
 catacaatgt taaataacct atttttttaa aaaagttcaa cttaaggtag 1850  
 aagttccaag ctactagtgt taaattggaa aatatcaata attaagagta 1900  
 ttttacccaa ggaatcctct catggaagtt tactgtgatg ttccttttct 1950  
 cacacaagtt ttagcctttt tcacaaggga actcatactg tctacacatc 2000  
 agaccatagt tgcttaggaa acctttaaaa attccagtta agcaatggtg 2050

aaatcagttt gcatctcttc aaaagaaacc tctcaggtta gctttgaact 2100  
 gcctcttcct gagatgacta ggacagtctg taccagagg ccaccagaa 2150  
 gccctcagat gtacatacac agatgccagt cagctcctgg gggtgcgcca 2200  
 ggcgcccccg ctctagctca ctgttgctc gctgtctgcc aggaggccct 2250  
 gccatccttg ggccttgga gtggctgtgt ccagtgagc ttactcacg 2300  
 tggcccttgc ttcattccagc acagctctca ggtgggcact gcaggacac 2350  
 tgggtgtcttc catgtagcgt ccagctttg ggctcctgta acagacctct 2400  
 ttttggttat ggatggctca caaataggg ccccaatgc ttttttttt 2450  
 ttttaagttt gtttaattat ttgttaagat tgtctaaggc caaaggcaat 2500  
 tgcgaaatca agtctgtcaa gtacaataac atttttaaaa gaaatggat 2550  
 cccactgttc ctctttgcca cagagaaagc acccagacgc cacaggctct 2600  
 gtcgcatttc aaaacaaacc atgatggagt ggcggccagt ccagcctttt 2650  
 aaagaacgtc aggtggagca gccaggtgaa aggcctggcg gggaggaaag 2700  
 tgaaacgcct gaatcaaaag cagttttcta attttgactt taaatttttc 2750  
 atccgccgga gacactgctc ccatttgagg ggggacatta gcaacatcac 2800  
 tcagaagcct gtgttcttca agagcagggtg ttctcagcct cacatgccct 2850  
 gccgtgctgg actcaggact gaagtgtgt aaagcaagga gctgctgaga 2900  
 aggagcactc cactgtgtgc ctggagaatg gctctcacta ctcacctgt 2950  
 ctttcagctt ccagtgtctt gggtttttta tactttgaca gctttttttt 3000  
 aattgcatac atgagactgt gttgactttt tttagttatg tgaaacactt 3050  
 tgccgcaggc cgctggcag aggcaggaaa tgctccagca gtggctcagt 3100  
 gctccctggg gtctgtgca tggcatcctg gatgcttagc atgcaagttc 3150  
 cctccatcat tgccaccttg gtagagaggg atggctcccc accctcagcg 3200  
 ttggggattc acgctccagc ctcttcttg gttgtcatag tgatagggt 3250  
 gccttattgc cccctcttct tataacctaa aaccttctac actagtcca 3300  
 tgggaaccag gtctgaaaaa gtagagagaa gtgaaagtag agtctgggaa 3350  
 gtagctgcct ataactgaga ctagacggaa aaggaatact cgtgtatttt 3400

aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450  
 gcctttggat ggatggttgc gtacacagat gctacagact tgtactaaca 3500  
 caccgtaatt tggcatttgc ttaacctcat ttataaaagc ttcaaaaaaa 3550  
 ccca 3554

<210> 423  
 <211> 310  
 <212> PRT  
 <213> Homo Sapien

<400> 423

Met	Ala	Leu	Arg	Arg	Pro	Pro	Arg	Leu	Arg	Leu	Cys	Ala	Arg	Leu	1	5	10	15
Pro	Asp	Phe	Phe	Leu	Leu	Leu	Leu	Phe	Arg	Gly	Cys	Leu	Ile	Gly	20	25	30	
Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu	35	40	45	
Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr	50	55	60	
Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr	65	70	75	
Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly	80	85	90	
Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val	95	100	105	
Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg	110	115	120	
Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val	125	130	135	
Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val	140	145	150	
Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly	155	160	165	
His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu	170	175	180	
Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe	185	190	195	

090916.0004

His	Leu	Asn	Ser	Glu	Thr	Gly	Thr	Leu	Val	Phe	Thr	Ala	Val	His
				200					205					210
Lys	Asp	Asp	Ser	Gly	Gln	Tyr	Tyr	Cys	Ile	Ala	Ser	Asn	Asp	Ala
				215					220					225
Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu
				230					235					240
Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val
				245					250					255
Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly
				260					265					270
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
				275					280					285
Gly	Lys	Pro	Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly
				290					295					300
Asp	Phe	Arg	His	Lys	Ser	Ser	Phe	Val	Ile					
				305					310					

090904-0740